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OM nucleic - nucleic search, using sw model

Run on: January 9, 2003, 10:50:19 ; Search time 6156 seconds
(without alignments)
11213.752 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcaacgcgcgagcttgctg.....attacagcgcgacccaccg 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pi.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_on.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pi.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB | ID | Description |
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| 2 | 2372 | 100.0 | 2372 | 6 | AR009781 | Sequence AR009781 |
| 3 | 2372 | 100.0 | 2372 | 6 | AR028963 | Sequence AR028963 |
| 4 | 2372 | 100.0 | 2372 | 6 | AR154584 | Sequence AR154584 |
| 5 | 2372 | 100.0 | 2372 | 6 | AR212312 | Sequence AR212312 |
| 6 | 2372 | 100.0 | 2372 | 6 | AX329941 | Sequence AX329941 |
| 7 | 2372 | 100.0 | 2372 | 6 | I11727 | Sequence I11727 |
| 8 | 2372 | 100.0 | 2372 | 6 | I12226 | Sequence I12226 |
| 9 | 2372 | 100.0 | 2372 | 6 | I21256 | Sequence I21256 |
| 10 | 2372 | 100.0 | 2372 | 6 | I25341 | Sequence I25341 |
| 11 | 2372 | 100.0 | 2372 | 6 | I36472 | Sequence I36472 |
| 12 | 2372 | 100.0 | 2372 | 6 | I40222 | Sequence I40222 |
| 13 | 2372 | 100.0 | 2372 | 6 | I79856 | Sequence I79856 |
| 14 | 2372 | 100.0 | 2372 | 6 | I86850 | Sequence I86850 |
| 15 | 2372 | 100.0 | 2372 | 9 | HSP53ASSG | Sequence Z12020 H.sapiens m |
| 16 | 2372 | 100.0 | 2372 | 9 | HUMSP53A | Sequence M92424 Human p53-a |
| 17 | 2061.4 | 86.9 | 3130 | 9 | BC009893 | Sequence BC009893 Homo sapi |
| 18 | 1476 | 62.2 | 1476 | 6 | A61359 | Sequence A61359 |
| 19 | 1476 | 62.2 | 1476 | 6 | AX057138 | Sequence AX057138 |
| 20 | 1302 | 54.9 | 1302 | 6 | A44506 | Sequence A44506 |
| 21 | 1293.6 | 54.5 | 1476 | 4 | AF121140 | Sequence AF121140 Equus cab |
| 22 | 1288.6 | 54.3 | 1477 | 4 | AF322416 | Sequence AF322416 Canis fam |
| 23 | 1282.2 | 54.1 | 1469 | 4 | AB031276 | Sequence AB031276 Canis fam |
| 24 | 1278 | 53.9 | 1460 | 4 | AF100705 | Sequence AF100705 Canis fam |
| 25 | 1246 | 52.5 | 1391 | 9 | AF092845 | Sequence AF092845 Homo sapi |
| 26 | 1191.6 | 50.2 | 1564 | 4 | AF322417 | Sequence AF322417 Canis fam |
| 27 | 1186 | 50.0 | 1361 | 9 | AF092844 | Sequence AF092844 Homo sapi |
| 28 | 1127.4 | 47.5 | 14450 | 2 | AC026121 | Sequence AC026121 Homo sapi |
| 29 | 1127.4 | 47.5 | 145808 | 2 | AC016258 | Sequence AC016258 Homo sapi |
| 30 | 1127.4 | 47.5 | 150579 | 9 | AC025423 | Sequence AC025423 Homo sapi |
| 31 | 1127.4 | 47.5 | 173864 | 2 | AC078861 | Sequence AC078861 Homo sapi |
| 32 | 1127.4 | 47.5 | 179719 | 2 | AC124890 | Sequence AC124890 Homo sapi |
| 33 | 984.4 | 41.5 | 34088 | 9 | AF527840 | Sequence AF527840 Homo sapi |
| 34 | 977.2 | 41.2 | 1711 | 10 | MM040145 | Sequence U0145 Mus muscula |
| 35 | 975.6 | 41.1 | 1710 | 6 | AR000257 | Sequence AR000257 |
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| 37 | 975.6 | 41.1 | 1710 | 6 | AR028964 | Sequence AR028964 |
| 38 | 975.6 | 41.1 | 1710 | 6 | AR212313 | Sequence AR212313 |
| 39 | 975.6 | 41.1 | 1710 | 6 | AX305470 | Sequence AX305470 |
| 40 | 975.6 | 41.1 | 1710 | 6 | I11728 | Sequence I11728 |
| 41 | 975.6 | 41.1 | 1710 | 6 | I12227 | Sequence I12227 |
| 42 | 975.6 | 41.1 | 1710 | 6 | I21257 | Sequence I21257 |
| 43 | 975.6 | 41.1 | 1710 | 6 | I25342 | Sequence I25342 |
| 44 | 975.6 | 41.1 | 1710 | 6 | I36473 | Sequence I36473 |
| 45 | 975.6 | 41.1 | 1710 | 6 | I40223 | Sequence I40223 |

ALIGNMENTS

RESULT 1
AR000256
LOCUS AR000256 2372 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 2 from patent US 5736338.
ACCESSION AR000256
VERSION AR000256.1 GI:3962787
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.
TITLE Method of diagnosing Neoplastic disease by detecting increased
expression of human MDM2 protein
JOURNAL Patent: US 5736338-A 2 07-APR-1998;

FEATURES
source Location/Qualifiers
1. .2372
BASE COUNT 698 a 491 c 541 g 642 t
ORIGIN

Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2341 CAAAGTGTGGGATTTACAGGATGAGCCACCG 2372

RESULT 3
LOCUS AR028963
DEFINITION Sequence 2 from patent US 5858976.
ACCESSION AR028963
VERSION AR028963.1 GI:5940936
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM

Unclassified.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
TITLE Methods for inhibiting interaction of human MDM2 and p53
JOURNAL Patent: US 5858976-A 2 12-JAN-1999;
FEATURES Location/Qualifiers
source I. .2372
BASE COUNT 698 a 491 c 541 g 642 t
ORIGIN
Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTATATATTTTTTTTGG 2100
QY 2101 AGACCGAGCTTTGCTCTGTTTACCAGGCTGGAGTGCAGTGGTGGTCTTGGCTCACGTGCA 2160
Db 2101 AGACCGAGCTTTGCTCTGTTTACCAGGCTGGAGTGCAGTGGTGGTCTTGGCTCACGTGCA 2160
QY 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCTCAGCCCTCCCAATTTAGCTTGGCC 2220
Db 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCTCAGCCCTCCCAATTTAGCTTGGCC 2220
QY 2221 TACAGTCTATCTGCCACCACTGCTGCTAAATTTTGTACTTTTGTAGTACAGACAGGTTTC 2280
Db 2221 TACAGTCTATCTGCCACCACTGCTGCTAAATTTTGTACTTTTGTAGTACAGACAGGTTTC 2280
QY 2281 ACCGTGTTAGCAGGATGCTCTGATCTCTGACCTCGTATCGCCGACCTCGGCCCTCC 2340
Db 2281 ACCGTGTTAGCAGGATGCTCTGATCTCTGACCTCGTATCGCCGACCTCGGCCCTCC 2340
QY 2341 CAAAGTGTGGGATTTACAGGCATGAGCCACCG 2372
Db 2341 CAAAGTGTGGGATTTACAGGCATGAGCCACCG 2372

RESULT 4
ARI54584
LOCUS ARI54584 2372 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6238921.
ACCESSION ARI54584
VERSION ARI54584.1 GI:15122637
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Miraglia,L.J., Nero,P., Graham,M.J. and Monia,B.P.
TITLE Antisense oligonucleotide modulation of human mdm2 expression
JOURNAL Patent: US 6238921-A 1 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..2372
BASE COUNT 698 a 491 c 541 g 642 t
ORIGIN

Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTTGGCTTCTTGGGGCTGTGTGGCCCTGTGTGCGAAGATGGA 60
Db 1 GCACCGCGGAGCTTGGCTTCTTGGGGCTGTGTGGCCCTGTGTGCGAAGATGGA 60
QY 61 GCAAGAAGCCGAGCCGAGGGGCGCGACCCCTCTGACCGAGATCTCTGCTCTTCG 120
Db 61 GCAAGAAGCCGAGCCGAGGGGCGCGACCCCTCTGACCGAGATCTCTGCTCTTCG 120
QY 121 CAGCCAGGAGCACCCTCCCTCCCGGATTTAGTGCCTACGAGCGCCAGTGCCTGGCCCG 180
Db 121 CAGCCAGGAGCACCCTCCCTCCCGGATTTAGTGCCTACGAGCGCCAGTGCCTGGCCCG 180
QY 181 GAGAGTGGATGATCCCGAGGCCCGAGGGCTGCTGCTCCGAGTAGTCACTGCCCTG 240
Db 181 GAGAGTGGATGATCCCGAGGCCCGAGGGCTGCTGCTCCGAGTAGTCACTGCCCTG 240
QY 241 AAGGAACTGGGGAGTCTTTGAGGGACCCCGACTCCAAGCGGAAACCCCGGATGGA 300
Db 241 AAGGAACTGGGGAGTCTTTGAGGGACCCCGACTCCAAGCGGAAACCCCGGATGGA 300

| | | | | |
|----|------|---------------|--|------|
| QY | 301 | GGAGCAGGCAAA | TGTCGAATACCAACATGTCTGTACCTACTGATGGTGCTGTAACCACT | 360 |
| | | | | |
| Db | 301 | GGAGCAGGCAAA | TGCGAATATACCAACATGTCTGTACCTACTGATGGTGCTGTAACCACT | 360 |
| | | | | |
| QY | 361 | CACAGATTCCAGT | TTCGGAAACAGACACCTCGTTAGACCAAAAGCCATTGCTTTTGAAGT | 420 |
| | | | | |
| Db | 361 | CACAGATTCCAGT | TTCGGAAACAGACACCTCGTTAGACCAAAAGCCATTGCTTTTGAAGT | 420 |
| | | | | |
| QY | 421 | TATTAAAGTCTGT | TGTGTCNAAAAAGACATTAATCTATGAAGAGGTTCTTTTATC | 480 |
| | | | | |
| Db | 421 | TATTAAAGTCTGT | TGTGTCNAAAAAGACATTAATCTATGAAGAGGTTCTTTTATC | 480 |
| | | | | |
| QY | 481 | TTGGCCAGTATAT | TATGACTTAAACGATATATGATGAGAAGCAACATATGCTATATT | 540 |
| | | | | |
| Db | 481 | TTGGCCAGTATAT | TATGACTTAAACGATATATGATGAGAAGCAACATATGCTATATT | 540 |
| | | | | |
| QY | 541 | GTTCAAATGATCT | TCTAGGAGATTTGTTGGCGTGCCAAAGCTTCCTGTGAAGAGCACA | 600 |
| | | | | |
| Db | 541 | GTTCAAATGATCT | TCTAGGAGATTTGTTGGCGTGCCAAAGCTTCCTGTGAAGAGCACA | 600 |
| | | | | |
| QY | 601 | GGAAATATATAC | CATGATCTACAGAACTTGGTAGTGTCAATCAGCAGCAATCATCGG | 660 |
| | | | | |
| Db | 601 | GGAAATATATAC | CATGATCTACAGAACTTGGTAGTGTCAATCAGCAGCAATCATCGG | 660 |
| | | | | |
| QY | 661 | ACTCAGTACATCT | GAGTGAGACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGG | 720 |
| | | | | |
| Db | 661 | ACTCAGTACATCT | GAGTGAGACAGGTGTCACTTGAAGTGGGAGTGATCAAAAGG | 720 |
| | | | | |
| QY | 721 | ACCTTGTACAA | GAGTCTCAGGAAGAAACCTTCATCTCACATTTGGTTTCTAGACCAT | 780 |
| | | | | |
| Db | 721 | ACCTTGTACAA | GAGTCTCAGGAAGAAACCTTCATCTCACATTTGGTTTCTAGACCAT | 780 |
| | | | | |
| QY | 781 | CTACCTCATCTA | GAGGAGCAAAATTAGTGAGACAGAAAGAAATTCAGATGAATATCTG | 840 |
| | | | | |
| Db | 781 | CTACCTCATCTA | GAGGAGCAAAATTAGTGAGACAGAAAGAAATTCAGATGAATATCTG | 840 |
| | | | | |
| QY | 841 | GTGAACACAAAG | AAACGCCAAATCTGATAGTATTTCCCTTTCCCTTCATCAAGGCC | 900 |
| | | | | |
| Db | 841 | GTGAACACAAAG | AAACGCCAAATCTGATAGTATTTCCCTTTCCCTTCATCAAGGCC | 900 |
| | | | | |
| QY | 901 | TGGCTCTGTCTG | TATAAAGGGAGATATGTTGAAAGAGCAGTAGCAGTGAATCTACAG | 960 |
| | | | | |
| Db | 901 | TGGCTCTGTCTG | TATAAAGGGAGATATGTTGAAAGAGCAGTAGCAGTGAATCTACAG | 960 |
| | | | | |
| QY | 961 | GGAGCCATCGAAT | CCGGATCTTGATCTGGTGTAAGTGAACATTCAGGTGATGGTTGG | 1020 |
| | | | | |
| Db | 961 | GGAGCCATCGAAT | CCGGATCTTGATCTGGTGTAAGTGAACATTCAGGTGATGGTTGG | 1020 |
| | | | | |
| QY | 1021 | ATCAGGATTCA | GTTCAGATCAGTTTAGTGTAGAATTTGAAGTTGAATCTCTCGACTCAG | 1080 |
| | | | | |
| Db | 1021 | ATCAGGATTCA | GTTCAGATCAGTTTAGTGTAGAATTTGAAGTTGAATCTCTCGACTCAG | 1080 |
| | | | | |
| QY | 1081 | AAGATTATACCT | TACTGTAAGAGGACAAGACTCTCAGATGAAGATGATGAGGTATATC | 1140 |
| | | | | |
| Db | 1081 | AAGATTATACCT | TACTGTAAGAGGACAAGACTCTCAGATGAAGATGATGAGGTATATC | 1140 |
| | | | | |
| QY | 1141 | AAGTTACTGTGT | ATCAGCGAGGGAGGTGATACAGATTCATTTGAAGAAGATCCTGAAA | 1200 |
| | | | | |
| Db | 1141 | AAGTTACTGTGT | ATCAGCGAGGGAGGTGATACAGATTCATTTGAAGAAGATCCTGAAA | 1200 |
| | | | | |
| QY | 1201 | TTTCCCTTAGCT | GTATTTGGAAATGCACCTTCATGCAATGAATGAATCCCTCCCTCCAT | 1260 |
| | | | | |
| Db | 1201 | TTTCCCTTAGCT | GTATTTGGAAATGCACCTTCATGCAATGAATGAATCCCTCCCTCCAT | 1260 |
| | | | | |
| QY | 1261 | CACATTGCAAC | ACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCTGAAGATAAAGGGAAG | 1320 |
| | | | | |
| Db | 1261 | CACATTGCAAC | ACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCTGAAGATAAAGGGAAG | 1320 |
| | | | | |
| QY | 1321 | ATAAAGGGAAAT | CTCTGTAAGAGCCAAACTCGAAAACCTCAACACAAGCTGAAGAGGGCT | 1380 |
| | | | | |
| Db | 1321 | ATAAAGGGAAAT | CTCTGTAAGAGCCAAACTCGAAAACCTCAACACAAGCTGAAGAGGGCT | 1380 |
| | | | | |

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|----|------|-----------------------|----------|----------|---------|---------|-----------|------------|------|
| Qy | 1381 | TTGATGTTCTCTGATGTTGTA | AAAAAAAC | TATAGTGA | ATGATTC | CAGAGAG | TCATGTTG | TGAGG | 1444 |
| Db | 1381 | TTGATGTTCTCTGATGTTGTA | AAAAAAAC | TATAGTGA | ATGATTC | CAGAGAG | TCATGTTG | TGAGG | 1440 |
| Qy | 1441 | AAAAATGATGATAAAATTTAC | AAAGCTT | CAACAAT | CACAGAA | AGTGAAG | ACTATTTCT | CAGC | 1500 |
| Db | 1441 | AAAAATGATGATAAAATTTAC | AAAGCTT | CAACAAT | CACAGAA | AGTGAAG | ACTATTTCT | CAGC | 1500 |
| Qy | 1501 | CATCAACTTCTAGTAGCATTT | TTATAG | CAGCCAG | AGAGATG | TGAAGAG | TTTGAAG | AGG | 1560 |
| Db | 1501 | CATCAACTTCTAGTAGCATTT | TTATAG | CAGCCAG | AGAGATG | TGAAGAG | TTTGAAG | AGG | 1560 |
| Qy | 1561 | AAGAAACCCAAAGACAAAGA | GAGGTG | TGGAATCT | AGTTT | TGCCCTT | TAATGCC | ATTCAAC | 1620 |
| Db | 1561 | AAGAAACCCAAAGACAAAGA | GAGGTG | TGGAATCT | AGTTT | TGCCCTT | TAATGCC | ATTCAAC | 1620 |
| Qy | 1621 | CTTGTTGATTTTGTC | AAAGTGC | AGCTAA | AAATGGT | TGCATTT | GTCCATGG | CAAAACAG | 1680 |
| Db | 1621 | CTTGTTGATTTTGTC | AAAGTGC | AGCTAA | AAATGGT | TGCATTT | GTCCATGG | CAAAACAG | 1680 |
| Qy | 1681 | ATCTTATGGCCCTGCTTTAC | ATGTC | CAAGAG | AGCTAA | AGAAAGG | AAATGAAG | CCCTGCC | 1740 |
| Db | 1681 | ATCTTATGGCCCTGCTTTAC | ATGTC | CAAGAG | AGCTAA | AGAAAGG | AAATGAAG | CCCTGCC | 1740 |
| Qy | 1741 | TATGTAGACAAACCAATTT | CAATGAT | TGTGCT | AACCTTA | TTTCCCT | PAGTTG | ACCTGTCTAT | 1800 |
| Db | 1741 | TATGTAGACAAACCAATTT | CAATGAT | TGTGCT | AACCTTA | TTTCCCT | PAGTTG | ACCTGTCTAT | 1800 |
| Qy | 1801 | AAGAGAATTATATATTTCT | TAAC | TATATA | TACCCT | PAGAA | TTTAG | ACACCTG | 1860 |
| Db | 1801 | AAGAGAATTATATATTTCT | TAAC | TATATA | TACCCT | PAGAA | TTTAG | ACACCTG | 1860 |
| Qy | 1861 | CACATATATCAAGTGAG | AAAAATG | CCCTCA | ATTTC | CATAG | ATTCTCT | TTTAGTATA | 1920 |
| Db | 1861 | CACATATATCAAGTGAG | AAAAATG | CCCTCA | ATTTC | CATAG | ATTCTCT | TTTAGTATA | 1920 |
| Qy | 1921 | TGACCTACTTTTGGT | PAGTGA | ATAGTCA | ATTA | TGCTT | ACTATA | TTTGA | 1980 |
| Db | 1921 | TGACCTACTTTTGGT | PAGTGA | ATAGTCA | ATTA | TGCTT | ACTATA | TTTGA | 1980 |
| Qy | 1981 | CATGCTTTACACCAAC | TCCTAA | TTTTAA | ATAATTT | CTACT | CTGCTT | AAATGAGA | 2040 |
| Db | 1981 | CATGCTTTACACCAAC | TCCTAA | TTTTAA | ATAATTT | CTACT | CTGCTT | AAATGAGA | 2040 |
| Qy | 2041 | TTGGTTTTTTTTTCTT | AAATATG | TATG | ACATTA | TTAAATG | TAACTAT | TTTTTTTTT | 2100 |
| Db | 2041 | TTGGTTTTTTTTTCTT | AAATATG | TATG | ACATTA | TTAAATG | TAACTAT | TTTTTTTTT | 2100 |
| Qy | 2101 | AGACCGAGTCTTGCT | CTGTTT | ACCAGG | CTGGAG | TGCGAG | TGGGTG | ATCTTTGG | 2160 |
| Db | 2101 | AGACCGAGTCTTGCT | CTGTTT | ACCAGG | CTGGAG | TGCGAG | TGGGTG | ATCTTTGG | 2160 |
| Qy | 2161 | AGCTCTGCCCTCCCGGG | TCGCG | ACCAATTT | CTCCT | GCCTC | CAGCCT | CCCAATTTAG | 2220 |
| Db | 2161 | AGCTCTGCCCTCCCGGG | TCGCG | ACCAATTT | CTCCT | GCCTC | CAGCCT | CCCAATTTAG | 2220 |
| Qy | 2221 | TACAGTCATCTGCC | ACCAAC | ACCTTGG | CTAA | TTTTTT | TGTA | CTTTTAG | 2280 |
| Db | 2221 | TACAGTCATCTGCC | ACCAAC | ACCTTGG | CTAA | TTTTTT | TGTA | CTTTTAG | 2280 |
| Qy | 2281 | ACCGTGTTAG | CCAGATG | GTCTG | ATCT | CCCTG | ACCTCT | GTATCG | 2340 |
| Db | 2281 | ACCGTGTTAG | CCAGATG | GTCTG | ATCT | CCCTG | ACCTCT | GTATCG | 2340 |
| Qy | 2341 | CAAAAGTCTGGG | ATTAC | AGCAT | ATG | AGCC | ACCG | | 2372 |
| Db | 2341 | CAAAAGTCTGGG | ATTAC | AGCAT | ATG | AGCC | ACCG | | 2372 |

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|------------|
| RESULT 5 |
| AR212312 |
| LOCUS |
| DEFINITION |

2372 bp DNA linear PAT 20-JUN-2002
US 6399755.

Db 1861 CACATATATCAAAAGTGGAGAAATGCCCAATTACATAGATTCTTCTCTTAGTATAAT 1920
QY 1921 TGACCTACTTTGGTACTGGAAATAGTAACTACTTACTATAATTTGACTTGAATATAGACT 1980
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QY 2161 AGCTCTGCCCCCTCCCGGGTTCGCACCATTTCTCCTGCCTCAGCCTCCCAATTAGCTTGGCC 2220
Db 2161 AGCTCTGCCCCCTCCCGGGTTCGCACCATTTCTCCTGCCTCAGCCTCCCAATTAGCTTGGCC 2220
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Db 2221 TACAGTCATCTGCCACCTCCACCTGGCTTAATTTTGTACTTTTACTAGACAGGGTTTC 2280
QY 2281 ACCGTGTAGCCAGGATGCTCTCGATCTCCTGACCTCGTGTATCCGCCACCTCGGCCCTCC 2340
Db 2281 ACCGTGTAGCCAGGATGCTCTCGATCTCCTGACCTCGTGTATCCGCCACCTCGGCCCTCC 2340
QY 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372

RESULT 6
AX329941
LOCUS AX329941 2372 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 450 from Patent WO0194629.
ACCESSION AX329941
VERSION AX329941.1 GI:18102919
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 450 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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/db_xref="taxon:9606"
BASE COUNT 698 a 491 c 541 g 642 t
ORIGIN
Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCCGGGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGGAAGATGGA 60
Db 1 GCACCCGGGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGGAAGATGGA 60
QY 61 GCAAGAGCCGAGCCGAGGGGGCGCCGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
Db 61 GCAAGAGCCGAGCCGAGGGGGCGCCGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
QY 121 CAGCCAGGACCGCTCCCTCCCGGATTAGTGCGTACGAGCGCCCGCTGGCCCG 180

Db 121 CAGCCAGGACCGTCCCTCCCGGATTAGTGCGTACGAGCGCCAGTGCCTTGCCCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCCAGGGCGTGGTCTTCCCGAGTAGTCACTGCCCGTG 240
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QY 241 AAGGAAACTGGGAGTCTTGGAGGAGCCCGGAGCTCCCAAGCGCGAAGCCCGGATGGTGA 300
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QY 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACTACTGTATGTGTGTGTAAACCAT 360
Db 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACTACTGTATGTGTGTGTAAACCAT 360
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Db 361 CACAGATTCAGCTCCGGAACAGACACCTGGTTAGACAAGCCATTCCTTTTGAAGT 420
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QY 541 GTTCAATGATCTTCTAGGAGATTTGTTGGCGTGCACAGCTTCTCTGTAAGAGCACA 600
Db 541 GTTCAATGATCTTCTAGGAGATTTGTTGGCGTGCACAGCTTCTCTGTAAGAGCACA 600
QY 601 GGAATAATATACCATGATCTCAGGAACCTTGTGTAGTGTCAATCAGCAGGAATCATCG 660
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QY 661 ACTCAGTACATCTGTGAGTGAACAGAGTGTCACTTGAAGTGGAGTGAATCAAGG 720
Db 661 ACTCAGTACATCTGTGAGTGAACAGAGTGTCACTTGAAGTGGAGTGAATCAAGG 720
QY 721 ACCTTGTACAAGAGCTTTCAGGAAGAGAACTTCTCATCTTCAATTTGTTCTAGACCAT 780
Db 721 ACCTTGTACAAGAGCTTTCAGGAAGAGAACTTCTCATCTTCAATTTGTTCTAGACCAT 780
QY 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
Db 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
QY 841 GTGAACGACAAAGAAACGCCACAAATCTGATAGTATTTCCCTTTCTTGTGATGAAGCC 900
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QY 901 TGGCTCTGTGTGTAATGAAGGAGATATGTTGTGAAAGAGAGTGTAGTGTGATGATCTACAG 960
Db 901 TGGCTCTGTGTGTAATGAAGGAGATATGTTGTGAAAGAGAGTGTAGTGTGATGATCTACAG 960
QY 961 GGAGCCCATCGAATCCGGATCTTGTATGCTGGTGTAAAGTGAACATTCAGGTGTTGG 1020
Db 961 GGAGCCCATCGAATCCGGATCTTGTATGCTGGTGTAAAGTGAACATTCAGGTGTTGG 1020
QY 1021 ATCAGGATTCAGTTTTCAGATCAGTTTAGTGTAGAATTTGAAGTGTGATCTCGACTCAG 1080
Db 1021 ATCAGGATTCAGTTTTCAGATCAGTTTAGTGTAGAATTTGAAGTGTGATCTCGACTCAG 1080
QY 1081 AAGATTATAGCTTGTGAAAGAGGACAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
Db 1081 AAGATTATAGCTTGTGAAAGAGGACAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
QY 1141 AAGTACTGTGTATCAGGAGGAGAGTGTATCAGATTCATTGTAAGAGATCCCTGAA 1200
Db 1141 AAGTACTGTGTATCAGGAGGAGAGTGTATCAGATTCATTGTAAGAGATCCCTGAA 1200
QY 1201 TTTCTTGTAGTACTATGGAATGCAATTCATGCAATGAAATGAAATCCCTTCCAT 1260
Db 1201 TTTCTTGTAGTACTATGGAATGCAATTCATGCAATGAAATGAAATCCCTTCCAT 1260

[illegible]

| | | | |
|----|------|--|------|
| Qy | 661 | ACTCAGGTACATCTGTGAGTGAGAACAGAGTGTCACTTTGAAGGTGGAGTGATCAAAAGG | 720 |
| Db | 661 | ACTCAGGTACATCTGTGAGTGAGAACAGAGTGTCACTTTGAAGGTGGAGTGATCAAAAGG | 720 |
| Qy | 721 | ACCTTGTCACAGAGCTTTCAGGAGAGAACCTTCACTCTTCACATTTGGTTTCTAGACCAT | 780 |
| Db | 721 | ACCTTGTCACAGAGCTTTCAGGAGAGAACCTTCACTCTTCACATTTGGTTTCTAGACCAT | 780 |
| Qy | 781 | CTACCTCATCTACAAGGAGAGCAATTTAGTGTACACAGAAGAAAATTCAGATGAATATCTG | 840 |
| Db | 781 | CTACCTCATCTACAAGGAGAGCAATTTAGTGTACACAGAAGAAAATTCAGATGAATATCTG | 840 |
| Qy | 841 | GTGAACGACAAAGAAAACGCCCAAAATCTGATAGTATTTCCCTTTCTTTGATGAAGGCC | 900 |
| Db | 841 | GTGAACGACAAAGAAAACGCCCAAAATCTGATAGTATTTCCCTTTCTTTGATGAAGGCC | 900 |
| Qy | 901 | TGGCTCTGTGTGTAAATAAGGGAGATATGTTGTGAAGAAGCAGTAGCAGTGAATCTACAG | 960 |
| Db | 901 | TGGCTCTGTGTGTAAATAAGGGAGATATGTTGTGAAGAAGCAGTAGCAGTGAATCTACAG | 960 |
| Qy | 961 | GGAGCCCATCGAATCCGGATCTTTGATGCTGGTGTAAAGTGAACATTCAGGTGATTTGGTGG | 1020 |
| Db | 961 | GGAGCCCATCGAATCCGGATCTTTGATGCTGGTGTAAAGTGAACATTCAGGTGATTTGGTGG | 1020 |
| Qy | 1021 | ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGAATTTGAAGTTGAATCTCTCGACTCAG | 1080 |
| Db | 1021 | ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGAATTTGAAGTTGAATCTCTCGACTCAG | 1080 |
| Qy | 1081 | AAGATTATAGCCTTAGTGAAGAAGGACAGAACTCTCAGATGAAGATGAAGTATATC | 1140 |
| Db | 1081 | AAGATTATAGCCTTAGTGAAGAAGGACAGAACTCTCAGATGAAGATGAAGTATATC | 1140 |
| Qy | 1141 | AAGTTACTGTGTATCAGCAGGAGGAGTGATACAGATTCATTTGAAGAAGATCCTGAAA | 1200 |
| Db | 1141 | AAGTTACTGTGTATCAGCAGGAGGAGTGATACAGATTCATTTGAAGAAGATCCTGAAA | 1200 |
| Qy | 1201 | TTTTCCTTAGCTGACTATTGGAAATGCACCTTCATGCAATGAATGAATCCCCCTTCCAT | 1260 |
| Db | 1201 | TTTTCCTTAGCTGACTATTGGAAATGCACCTTCATGCAATGAATGAATCCCCCTTCCAT | 1260 |
| Qy | 1261 | CACATTCAACACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCTGGAAGATAAAGGGAAAG | 1320 |
| Db | 1261 | CACATTCAACACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCTGGAAGATAAAGGGAAAG | 1320 |
| Qy | 1321 | ATAAGGGGAAATCTCTGAGAAAGCCAACTGGAAAACCTCAACACAAGCTGAAGAGGGCT | 1380 |
| Db | 1321 | ATAAGGGGAAATCTCTGAGAAAGCCAACTGGAAAACCTCAACACAAGCTGAAGAGGGCT | 1380 |
| Qy | 1381 | TTGATGTCTTGATTCTAANAACCTATAGTGAATGATTTCCAGAGAGTCACTGTTGAGG | 1440 |
| Db | 1381 | TTGATGTCTTGATTCTAANAACCTATAGTGAATGATTTCCAGAGAGTCACTGTTGAGG | 1440 |
| Qy | 1441 | AAATGATGATAAAATACACAAGCTTCACAATCAACAAGAAGTGAAGACTATTTCTCAGC | 1500 |
| Db | 1441 | AAATGATGATAAAATACACAAGCTTCACAATCAACAAGAAGTGAAGACTATTTCTCAGC | 1500 |
| Qy | 1501 | CATCAACTCTCTAGTAGCATTTATTTATGACGCCAAGAAGATGTGAAGAGGTTGAAGAGG | 1560 |
| Db | 1501 | CATCAACTCTCTAGTAGCATTTATTTATGACGCCAAGAAGATGTGAAGAGGTTGAAGAGG | 1560 |
| Qy | 1561 | AAGAAACCCCAAGACAAGAGAGAGTGTGGATCTAGTTTCGCCCTTAATGCCATTTGAAC | 1620 |
| Db | 1561 | AAGAAACCCCAAGACAAGAGAGAGTGTGGATCTAGTTTCGCCCTTAATGCCATTTGAAC | 1620 |
| Qy | 1621 | CTTGTGTGATTTGTCGAAGTTCGACCTTAAAAATGGTTGCATTTGTCATGGCAAAACAGGAC | 1680 |
| Db | 1621 | CTTGTGTGATTTGTCGAAGTTCGACCTTAAAAATGGTTGCATTTGTCATGGCAAAACAGGAC | 1680 |
| Qy | 1681 | ATCTTTATGGCCTGCTTTACATGTGCAAGAGACTTAAAGAAAGGAATTAAGCCTTGCCAC | 1740 |
| Db | 1681 | ATCTTTATGGCCTGCTTTACATGTGCAAGAGAGCTTAAAGAAAGGAATTAAGCCTTGCCAC | 1740 |

| | | | |
|----|------|--|------|
| Qy | 1741 | TATCTAGACAAACCAATTCAAATGATGTGCTTAACCTTATTTCCCTAGTGTGACCTGCTCAT | 1800 |
| | | | |
| Db | 1741 | TATCTAGACAAACCAATTCAAATGATGTGCTTAACCTTATTTCCCTAGTGTGACCTGCTCAT | 1800 |
| | | | |
| Qy | 1801 | AAGAGAATATATATTTCTTAACCTATATAACCTAGGAATTTAGACAACCTGAAATTTATTT | 1860 |
| | | | |
| Db | 1801 | AAGAGAATATATATTTCTTAACCTATATAACCTAGGAATTTAGACAACCTGAAATTTATTT | 1860 |
| | | | |
| Qy | 1861 | CACATATATCAAAGTGGAGAAATGCCCAATTTACATAGATTTCTTCTCTTTAGTATAAAT | 1920 |
| | | | |
| Db | 1861 | CACATATATCAAAGTGGAGAAATGCCCAATTTACATAGATTTCTTCTCTTTAGTATAAAT | 1920 |
| | | | |
| Qy | 1921 | TGACCTACTTTGGTAGTGGAAATAGTGAATACATTTACTATAATTTGACTTGAAATGTAGCT | 1980 |
| | | | |
| Db | 1921 | TGACCTACTTTGGTAGTGGAAATAGTGAATACATTTACTATAATTTGACTTGAAATGTAGCT | 1980 |
| | | | |
| Qy | 1981 | CATCCTTTACACCAACTCCCTAAATTTTAAATAAATTTCTACTCTGTCTTAAATGAGAACTAC | 2040 |
| | | | |
| Db | 1981 | CATCCTTTACACCAACTCCCTAAATTTTAAATAAATTTCTACTCTGTCTTAAATGAGAACTAC | 2040 |
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| Qy | 2041 | TGTGTTTTTTTTTTCTTAAATATGTATATGACATTTAAATGTAACCTATTATTTTTTTTGT | 2100 |
| | | | |
| Db | 2041 | TGTGTTTTTTTTTTCTTAAATATGTATATGACATTTAAATGTAACCTATTATTTTTTTTGT | 2100 |
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| Qy | 2101 | AGACCGAGTCTTGCTCTGTATACCGAGCTGGAGTCGAGTGGTGATCTTGCTCCTCACTGCA | 2160 |
| | | | |
| Db | 2101 | AGACCGAGTCTTGCTCTGTATACCGAGCTGGAGTCGAGTGGTGATCTTGCTCCTCACTGCA | 2160 |
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| Qy | 2161 | AGCTCTGCCCTCCCGGGTTTCGCACCATTTCTCCTGCCCTCAGCCTCCCAATTAGCTTGGCC | 2220 |
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| Db | 2161 | AGCTCTGCCCTCCCGGGTTTCGCACCATTTCTCCTGCCCTCAGCCTCCCAATTAGCTTGGCC | 2220 |
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| Qy | 2221 | TACAGTCATCTGCCACACACACTGGGCTAAATTTTTTGTACTTTTGTAGTAGACAGAGGGTTTC | 2280 |
| | | | |
| Db | 2221 | TACAGTCATCTGCCACACACACTGGGCTAAATTTTTTGTACTTTTGTAGTAGACAGAGGGTTTC | 2280 |
| | | | |
| Qy | 2281 | ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGCGCTCC | 2340 |
| | | | |
| Db | 2281 | ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCACCTCGCGCTCC | 2340 |
| | | | |
| Qy | 2341 | CAAAAGTCTGGGATTAACAGCATGAGCCACCG | 2372 |
| | | | |
| Db | 2341 | CAAAAGTCTGGGATTAACAGCATGAGCCACCG | 2372 |
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| LOCUS | I12226 |
| DEFINITION | Sequence 1 from patent US 5420263. |
| ACCESSION | I12226 |
| VERSION | I12226.1 GI:909724 |
| KEYWORDS | . Unknown. |
| SOURCE | Unknown. |
| ORGANISM | Unclassified. |
| REFERENCE | 1 (bases 1 to 2372) |
| AUTHORS | Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B. |
| TITLE | Amplification of human MDM2 gene in human tumors |
| JOURNAL | Patent: US 5420263-A 1 30-MAY-1995; |
| FEATURES | Location/Qualifiers 1..2372 /organism="unknown" |
| BASE COUNT | 698 a 491 c 541 g 642 t |
| ORIGIN | |

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| | | | | Gaps | 0: |
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| DB | 1 | GCACGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGAAAGATGGA | 60 | | |

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 QY 1921 TGACCTACTTTGGTAGTGAATAGTGAATTTACTATTAATTTGACTTTGAATATGTAGCT 1980
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RESULT 9

LOCUS 121256 2372 bp DNA linear PAT 07-OCT-1996

DEFINITION Sequence 1 from patent US 5519118.

ACCESSION 121256

VERSION 121256.1 GI:1601610

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2372)

AUTHORS Vogelstein,B. and Kinzler,K.

TITLE Human MDM2 protein involved in human tumors

JOURNAL Patent: US 5519118-A 1 21-MAY-1996;

FEATURES

Location/Qualifiers

1..2372

source /organism="unknown"

BASE COUNT 698 a 491 c 541 g 642 t

ORIGIN

Query Match 100.0%; Score 2372; DB 6; Length 2372;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCGCAGCTTGCTGCTCTGCGGCGCTGTGGCCCTGTGGCCCTGTGTCGGAAGATGGA 60

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Qy 61 GCAAGAACCGAGCCGAGGCGCGCGCCGACCCCTCTGACCGAGATCCTGCTGCTTTTCG 120

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Qy 121 CAGCAGGAGCAGCTCCCTCCCGGATAGTGCCTACGAGCGCCAGTCCCTGCGCCG 180

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Qy 181 GAGAGTGGAATGATCCCGAGGCCCGCGCTGCTCTCCGAGTAGTCACTCCCGCTG 240

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RESULT 11
136472
LOCUS 136472
DEFINITION Sequence 2 from patent US 5606044.
ACCESSION 136472
VERSION 136472.1
GI:2086985
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.
TITLE Kits for detecting amplification of human MDM2
JOURNAL Patent: US 5606044-A 2 25-FEB-1997;
FEATURES
 location/Qualifiers
 1. 2372
 source
 BASE COUNT 698 a 491 c 541 g 642 t
 ORIGIN

Query Match 100.0%; Score 2372; DB 6; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 12
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ACCESSION I40222
VERSION I40222.1 GI:2083227
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2372)
AUTHORS Burrell, M., Hill, D.E., Kinzler, K.W. and Vogelstein, B.
TITLE Antibodies for detection of human MDM2 protein
JOURNAL Patent: US 5618921-A 2 08-APR-1997;
FEATURES Location/Qualifiers
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 REFERENCE Unclassified.
 1 (bases 1 to 2372)
 AUTHORS Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B.
 TITLE Polypeptides which bind to human MDM2
 JOURNAL Patent: US 5708136-A 2 13-JAN-1998;
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2372)
 AUTHORS Oliner, J.D., Kinzler, K.W., Meltzer, P.S., George, D.L. and Vogelstein, B.
 TITLE Amplification of a gene encoding a p53-associated protein in human sarcomas
 JOURNAL Nature 358 (6381), 80-83 (1992)
 MEDLINE 92310576
 PUBMED 1614537
 REFERENCE 2 (bases 1 to 2372)
 AUTHORS Kinzler, K.
 TITLE Direct Submission
 JOURNAL Submitted (29-APR-1992) Kinzler K., Johns Hopkins School of Medicine, 424 North Bond Street, Baltimore, MD, U.S.A

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| DB | 661 | ACTCAGGTACATCTGTGAGTGAAGAGGTGTCACCTTGAAGGTGGAGTGATCAAAAG | 720 | | | | |
| QY | 721 | ACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTACATTTGTTTCTAGACCAT | 780 | | | | |
| DB | 721 | ACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATCTTACATTTGTTTCTAGACCAT | 780 | | | | |
| QY | 781 | CTACCTCATCTAGAGGAGCAATTAGTGAGACAGAAATTCAGATGAATATCTG | 840 | | | | |
| DB | 781 | CTACCTCATCTAGAGGAGCAATTAGTGAGACAGAAATTCAGATGAATATCTG | 840 | | | | |
| QY | 841 | GTGAAGGACAAAGAAACGCCAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC | 900 | | | | |
| DB | 841 | GTGAAGGACAAAGAAACGCCAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC | 900 | | | | |
| QY | 901 | TGGCTCTGTGTAAAGGAGATATGTTGTAAGAGAGCAGTAGCAGTGAATCTACAG | 960 | | | | |
| DB | 901 | TGGCTCTGTGTAAAGGAGATATGTTGTAAGAGAGCAGTAGCAGTGAATCTACAG | 960 | | | | |
| QY | 961 | GGAGCCATCGAATCCGGATCTTGATGCTGGGTGAAGTGAACATTCAGGTGATGGTTGG | 1020 | | | | |
| DB | 961 | GGAGCCATCGAATCCGGATCTTGATGCTGGGTGAAGTGAACATTCAGGTGATGGTTGG | 1020 | | | | |


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|||||
Db 2101 AGACCGAGTCTTGCTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTTGGCTCAGTGCA 2160
Qy 2161 AGCTCTGCCCTCCCGGGTTCCGCACCATCTCTCTGCTCAGCTCCCAATTTAGCTTGGCC 2220
Db 2161 AGCTCTGCCCTCCCGGGTTCCGCACCATCTCTCTGCTCAGCTCCCAATTTAGCTTGGCC 2220
Qy 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTTTTTGTACTTTTAGTAGAGACAGGGTTTC 2280
Db 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTTTTTGTACTTTTAGTAGAGACAGGGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCCTCC 2340
Db 2281 ACCGTGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTCGGCCCTCC 2340
Qy 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

```

Search completed: January 9, 2003, 12:43:32
Job time : 6162 secs

XX
PA
UNITED STATES OF AMERICA

PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;
XX WPI: 1993-336944/42.
DR P-PSDB; AAR42175.
XX Diagnosing neoplasia from amplification of MDM2 gene - or
PT elevated gene expression, also new DNA, MDM2 protein, antibodies
PT and treatment of sarcoma by inhibiting MDM2 expression
XX Claim 19; Fig 1; 75pp; English.
XX This sequence represents the MDM2 gene. Amplification of this gene is
CC diagnostic of neoplasia or the potential for neoplasia. The protein
CC encoded by this gene interacts with the product of the p53 gene. p53
CC is a tumour suppressor gene and encodes a protein which appears to be
CC a member of a group of proteins which regulate normal cellular
CC proliferation and suppression of cellular transformation. Inactivation
CC of the p53 gene has been implicated in the formation, or progression of
CC a wide variety of carcinoma. Polypeptides containing at least amino
CC acids 13-41 of p53, or the DNA encoding these, may be used to inhibit
CC the growth of tumour cells containing MDM2 gene amplification.
XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
SQ
Query Match 100.0%; Score 2372; DB 14; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGGAGCTGGCTCTCTGGGGCTGTGGCCCTGTGTGTCGGAAGATGA 60
DB 1 GCACCGCGGAGCTGGCTCTCTGGGGCTGTGTGGCCCTGTGTGTCGGAAGATGA 60
QY 61 GCAGAGCCGAGCCGAGGGGGCGCCGACCCCTCTGACCGAGATCTGTGCTTTCG 120
DB 61 GCAGAGCCGAGCCGAGGGGGCGCCGACCCCTCTGACCGAGATCTGTGCTTTCG 120
QY 121 CAGCCAGGAGCACCCTCCCTCCCGGATTAGTGGTACGAGCCGACCTGCTGCCCTGCCCG 180
DB 121 CAGCCAGGAGCACCCTCCCTCCCGGATTAGTGGTACGAGCCGACCTGCTGCCCTGCCCG 180
QY 181 GAGAGTGGAGTATCCCGAGGCCCGAGGGCGTGTGCTCCGAGTAGTCAGTCCCGTG 240
DB 181 GAGAGTGGAGTATCCCGAGGCCCGAGGGCGTGTGCTCCGAGTAGTCAGTCCCGTG 240
QY 241 AAGGAACTGGGAGCTTTGAGGACCCCGGACTCCAGCGGAAACCCCGGATGGTGA 300
DB 241 AAGGAACTGGGAGCTTTGAGGACCCCGGACTCCAGCGGAAACCCCGGATGGTGA 300
QY 301 GGAGCAGGCAATGTCGAATACCAACATGCTGTACCTACTGATGGTGTAAACCACT 360
DB 301 GGAGCAGGCAATGTCGAATACCAACATGCTGTACCTACTGATGGTGTAAACCACT 360
QY 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGGCCATTTCTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGGCCATTTCTTTGAAGT 420
QY 421 TATTAAGTCTCTGGTCACAAAAGACACTTATATATGATGAAAGAGGTTCTTTTATC 480
DB 421 TATTAAGTCTCTGGTCACAAAAGACACTTATATATGATGAAAGAGGTTCTTTTATC 480
QY 481 TTGGCCAGTATATGACTAAACGATTATATGATGAGAACCAACATATTGTATATT 540
DB 481 TTGGCCAGTATATGACTAAACGATTATATGATGAGAACCAACATATTGTATATT 540
QY 541 GTTCAATGATCTTCTAGGAGATTGTTGGCGTCCCAAGCTTCTCTGTGAAAGACACA 600
DB 541 GTTCAATGATCTTCTAGGAGATTGTTGGCGTCCCAAGCTTCTCTGTGAAAGACACA 600
QY 601 GGAAATATATACCATGATCTACAGGAATGGTAGTAGTCAATCAGCAGGAATCATCG 660
DB 601 GGAAATATATACCATGATCTACAGGAATGGTAGTAGTCAATCAGCAGGAATCATCG 660
QY 661 ACTCAGGTACATCTGTGAGTGAGACAGGTGTACCTTGAAGTGGAGTGATCAAAAG 720

DB 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTACCTTGAAGTGGAGTGATCAAAAG 720
QY 721 ACCTTGTACAAGAGCTTTCAGGAAGAGAAACCTTCTATCTTACATTTGGTTTCTAGACCAT 780
DB 721 ACCTTGTACAAGAGCTTTCAGGAAGAGAAACCTTCTATCTTACATTTGGTTTCTAGACCAT 780
QY 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGACAGAGAAATTCAGATGAATTTATCTG 840
DB 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGACAGAGAAATTCAGATGAATTTATCTG 840
QY 841 GTGAAGCAACAAGAAACCCACAAATCTGTAGTAGTATTTCCCTTTCTTTGATGAAAGCC 900
DB 841 GTGAAGCAACAAGAAACCCACAAATCTGTAGTAGTATTTCCCTTTCTTTGATGAAAGCC 900
QY 901 TGGCTCTGTGTGTAAAGGGAGATATGTTGGAAGAGCAGTAGCAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTGTAAAGGGAGATATGTTGGAAGAGCAGTAGCAGTGAATCTACAG 960
QY 961 GGAGCCCATCGAATCCGGATCTTTGATGCTGGTGTAAAGTGAACATTCAGGTGATTTGGTGG 1020
DB 961 GGAGCCCATCGAATCCGGATCTTTGATGCTGGTGTAAAGTGAACATTCAGGTGATTTGGTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAGAATTTGAAAGTGAATCTCTCCACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAGAATTTGAAAGTGAATCTCTCCACTCAG 1080
QY 1081 AAGATTATAGCCCTTGTAGTGAAGAGGACAAAGACTCTCAGATGAAGATGATGAGGTATATC 1140
DB 1081 AAGATTATAGCCCTTGTAGTGAAGAGGACAAAGACTCTCAGATGAAGATGATGAGGTATATC 1140
QY 1141 AAGTTACTGTGTATCAGGAGGGAGAGTATACAGATTCATTTGAAGAAGATCCTGAAA 1200
DB 1141 AAGTTACTGTGTATCAGGAGGGAGAGTATACAGATTCATTTGAAGAAGATCCTGAAA 1200
QY 1201 TTTCCCTTAGCTGACTATTGGAAATGCATTCATGCAATGAAATGAATCCCTCCCTTCCAT 1260
DB 1201 TTTCCCTTAGCTGACTATTGGAAATGCATTCATGCAATGAAATGAATCCCTCCCTTCCAT 1260
QY 1261 CACATTCACACAGATCTGGGCCCTTCGTGAGAAATGCTTCCCTGAGATGAAGAGGAAG 1320
DB 1261 CACATTCACACAGATCTGGGCCCTTCGTGAGAAATGCTTCCCTGAGATGAAGAGGAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAAGAACTCAACACAAAGCTGAAGAGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAAGAACTCAACACAAAGCTGAAGAGGCT 1380
QY 1381 TTGATGTTCTGTGATTAAGAAACCTATAGTCAATGATTCAGAGAGTATGTTGAGG 1440
DB 1381 TTGATGTTCTGTGATTAAGAAACCTATAGTCAATGATTCAGAGAGTATGTTGAGG 1440
QY 1441 AAAATGATGATAAATTTACACAGCTTCAACATCAACAGAAAGTGAAGACTATTCTCAGC 1500
DB 1441 AAAATGATGATAAATTTACACAGCTTCAACATCAACAGAAAGTGAAGACTATTCTCAGC 1500
QY 1501 CATCACTCTCTAGTACATTTATTTAGCAGCCAAAGAGATGTGAAAGAGTTTGAAGAGG 1560
DB 1501 CATCACTCTCTAGTACATTTATTTAGCAGCCAAAGAGATGTGAAAGAGTTTGAAGAGG 1560
QY 1561 AAGAAACCCCAAGCAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAAATGCCATTGAAC 1620
DB 1561 AAGAAACCCCAAGCAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAAATGCCATTGAAC 1620
QY 1621 CTTGTGTGATTTCTCAAGGTCGACCTTAAATGTTGATTTGCTCCATGGCAAAACAGAC 1680
DB 1621 CTTGTGTGATTTCTCAAGGTCGACCTTAAATGTTGATTTGCTCCATGGCAAAACAGAC 1680
QY 1681 ATCTTATGGCTCTTTTACATGTGCAAGAGACTAAAGAAAGGAATTAAGCCCTGCCAG 1740
DB 1681 ATCTTATGGCTCTTTTACATGTGCAAGAGACTAAAGAAAGGAATTAAGCCCTGCCAG 1740
QY 1741 TATGTAGACACCAATTCAAATGATGTCTAACTTATTTCCCTTAGTTGACCTGTCTAT 1800

| | | | |
|----|------|--|------|
| Db | 1741 | TATGTAGACAAACAATTCAAATGATGTGCTAACATTATTTCCCTAGTTGACCTGTCTAT | 1800 |
| Qy | 1801 | AAGAGAAATATATATTTCTAACTATATAACCTTAGGAATTTAGACAACCTGAAATTTATT | 1860 |
| Db | 1801 | AAGAGAAATATATATTTCTAACTATATAACCTTAGGAATTTAGACAACCTGAAATTTATT | 1860 |
| Qy | 1861 | CACATATCAAGTGAGAAAAAGCCTCAATTCACATAGATTTCTCTTTAGTATAAT | 1920 |
| Db | 1861 | CACATATCAAGTGAGAAAAAGCCTCAATTCACATAGATTTCTCTTTAGTATAAT | 1920 |
| Qy | 1921 | TGACCTACTTTGGTAGTGGAAATAGTGAATACTATAATTTGACTTTGAATATGTAGCT | 1980 |
| Db | 1921 | TGACCTACTTTGGTAGTGGAAATAGTGAATACTATAATTTGACTTTGAATATGTAGCT | 1980 |
| Qy | 1981 | CATCTTTACACCAACTCCTAAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC | 2040 |
| Db | 1981 | CATCTTTACACCAACTCCTAAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC | 2040 |
| Qy | 2041 | TTGGTTTTTTTTTCTTAAATATGATATAGCATTTAAATGTAACCTATTATTTTTTTTG | 2100 |
| Db | 2041 | TTGGTTTTTTTTTCTTAAATATGATATAGCATTTAAATGTAACCTATTATTTTTTTTG | 2100 |
| Qy | 2101 | AGACCGAGTCTGCTCTGTTACCCAGGCTGGAGTGCAGTGGTGATCTTGGCTCACGTCA | 2160 |
| Db | 2101 | AGACCGAGTCTGCTCTGTTACCCAGGCTGGAGTGCAGTGGTGATCTTGGCTCACGTCA | 2160 |
| Qy | 2161 | AGCTCTGCCCTCCCGGGTTCGCACCAATCTCCTGCCCTCAGCCTGCCAATTTAGCTTGGCC | 2220 |
| Db | 2161 | AGCTCTGCCCTCCCGGGTTCGCACCAATCTCCTGCCCTCAGCCTGCCAATTTAGCTTGGCC | 2220 |
| Qy | 2221 | TACAGTCATCTGCCACCACACCTGGGTAAATTTTTTGTACTTTTAGTAGAGACAGGGTTTC | 2280 |
| Db | 2221 | TACAGTCATCTGCCACCACACCTGGGTAAATTTTTTGTACTTTTAGTAGAGACAGGGTTTC | 2280 |
| Qy | 2281 | ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCTGTGATCCGCCCAACCTCGGCCTCC | 2340 |
| Db | 2281 | ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCTGTGATCCGCCCAACCTCGGCCTCC | 2340 |
| Qy | 2341 | CAAAGTCTGGGATTACAGGCATGAGCCACCG | 2372 |
| Db | 2341 | CAAAGTCTGGGATTACAGGCATGAGCCACCG | 2372 |

RESULT 2

[illegible]

Db 721 ACCCTGACAGAGCTTCAGAGAGAAACCTTCATCTTCACATTTGGTTCTAGACCAT 780
 Qy 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGAGAAATTTAGATGAATTTATCTG 840
 Db 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGAGAAATTTAGATGAATTTATCTG 840
 Qy 841 GTGAACGACAAAGAAAGCCACAAATCTGATAGTATTTCCCTTCCCTTTGATGAAGCC 900
 Db 841 GTGAACGACAAAGAAAGCCACAAATCTGATAGTATTTCCCTTCCCTTTGATGAAGCC 900
 Qy 901 TGGCTCTGTGTGTAATAGGAGATGTTGTGAAGAGCAGTACAGTGAATCTACAG 960
 Db 901 TGGCTCTGTGTGTAATAGGAGATGTTGTGAAGAGCAGTACAGTGAATCTACAG 960
 Qy 961 GGAGCCCATCGAATCCGGATCTTGATGCTGGTGTAAAGTGAACATTCAGGTGATGGTGG 1020
 Db 961 GGAGCCCATCGAATCCGGATCTTGATGCTGGTGTAAAGTGAACATTCAGGTGATGGTGG 1020
 Qy 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGTAGATTTGAAGTGAATCTCAGACTCAG 1080
 Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGTAGATTTGAAGTGAATCTCAGACTCAG 1080
 Qy 1081 AAGATTATAGCTTTAGTGAAGAGGAGCAAGAACTCTCAGATGAAGTATGATGAGTATATC 1140
 Db 1081 AAGATTATAGCTTTAGTGAAGAGGAGCAAGAACTCTCAGATGAAGTATGATGAGTATATC 1140
 Qy 1141 AAGTTACTGTATCAGGAGGAGAGTATACAGATTCATTTGAAGAGATCCCTGAA 1200
 Db 1141 AAGTTACTGTATCAGGAGGAGAGTATACAGATTCATTTGAAGAGATCCCTGAA 1200
 Qy 1201 TTTCTTTAGCTGACTATTTGGAATGCACTTCATGCAATGAATGAATCCCTCCCTTCCAT 1260
 Db 1201 TTTCTTTAGCTGACTATTTGGAATGCACTTCATGCAATGAATGAATCCCTCCCTTCCAT 1260
 Qy 1261 CACATTCGAACAGATTTGGGCCCCCTCGTGAGAAATTTGGCTTCCTGAAAGTAAAGGAAAG 1320
 Db 1261 CACATTCGAACAGATTTGGGCCCCCTCGTGAGAAATTTGGCTTCCTGAAAGTAAAGGAAAG 1320
 Qy 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAGCTGGAAGGGCT 1380
 Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAGCTGGAAGGGCT 1380
 Qy 1381 TTGATGTTCTGATTTGAAAAAAGTATAGTGAATGATTTCCAGAGAGTATGTTGAGG 1440
 Db 1381 TTGATGTTCTGATTTGAAAAAAGTATAGTGAATGATTTCCAGAGAGTATGTTGAGG 1440
 Qy 1441 AAAATGATGATAAAATACAAAGCTTCACAAATCAGAAAGTGAAGTATTTCTCAGC 1500
 Db 1441 AAAATGATGATAAAATACAAAGCTTCACAAATCAGAAAGTGAAGTATTTCTCAGC 1500
 Qy 1501 CATCAACTCTAGTAGCATTATTTATAGCAGCCAAAGAGTGTGAAGAGTTTGAAGGG 1560
 Db 1501 CATCAACTCTAGTAGCATTATTTATAGCAGCCAAAGAGTGTGAAGAGTTTGAAGGG 1560
 Qy 1561 AAGAAACCCCAAGACAGAGTGTGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
 Db 1561 AAGAAACCCCAAGACAGAGTGTGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
 Qy 1621 CTTGTGTGATTTGTCAAGGTGCACTTAAATGTTTGCATTTGCCATGGCAAAACAGGAC 1680
 Db 1621 CTTGTGTGATTTGTCAAGGTGCACTTAAATGTTTGCATTTGCCATGGCAAAACAGGAC 1680
 Qy 1681 ATCTTATGGCTGCTTTACATGTCGAAAGTAAAGTAAAGAAAGAAATAGCCCTGCCAG 1740
 Db 1681 ATCTTATGGCTGCTTTACATGTCGAAAGTAAAGTAAAGAAAGAAATAGCCCTGCCAG 1740
 Qy 1741 TATGTAGACAAACCAATTCATGCTGCTTAACTTATTTCCCTAGTTGACCTGCTAT 1800
 Db 1741 TATGTAGACAAACCAATTCATGCTGCTTAACTTATTTCCCTAGTTGACCTGCTAT 1800
 Qy 1801 AAGAGAAATATATTTCTAACTATATAACCTTAGGAATTTAGACAACTGAAATTTAT 1860
 Db 1801 AAGAGAAATATATTTCTAACTATATAACCTTAGGAATTTAGACAACTGAAATTTAT 1860

Db 1801 AAGAGAAATATATTTCTAACTATATAACCTTAGGAATTTAGACAACTGAAATTTAT 1860
 Qy 1861 CACATATATCAAGTGAGAAAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAT 1920
 Db 1861 CACATATATCAAGTGAGAAAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAT 1920
 Qy 1921 TGACCTACTTTGGTAGTGAATAGTGAATCTACTATAAATTTGACTTGAATATAGT 1980
 Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATCTACTATAAATTTGACTTGAATATAGT 1980
 Qy 1981 CATCTTTTACACCAACTCCTAAATTTAAATAATTTCTACTGTCTTAAATGAGAAGTAC 2040
 Db 1981 CATCTTTTACACCAACTCCTAAATTTAAATAATTTCTACTGTCTTAAATGAGAAGTAC 2040
 Qy 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTG 2100
 Db 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTG 2100
 Qy 2101 AGACCGAGTCTTGGCTCTGTACCCAGGCTGGAGTGCAGTGGGTGATCTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTTGGCTCTGTACCCAGGCTGGAGTGCAGTGGGTGATCTGGCTCACTGCA 2160
 Qy 2161 AGCTCTGCCCTCCCGGGTTCCGACCACTTCTCTGCCCTCAGCTCCCAATTAGCTTGSCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTCCGACCACTTCTCTGCCCTCAGCTCCCAATTAGCTTGSCC 2220
 Qy 2221 TACAGTCATCTGCCACCACTGGCTGAATTTTTTGTACTTTTAGTAGACAGGGTTTC 2280
 Db 2221 TACAGTCATCTGCCACCACTGGCTGAATTTTTTGTACTTTTAGTAGACAGGGTTTC 2280
 Qy 2281 ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGGCCCTCC 2340
 Db 2281 ACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGGCCCTCC 2340
 Qy 2341 CAAAGTGTGGGATTACAGGCATGAGCCACCG 2372
 Db 2341 CAAAGTGTGGGATTACAGGCATGAGCCACCG 2372

RESULT 3
 AAT45151
 ID AAT45151 standard; cDNA; 2372 BP.
 XX AAT45151;
 AC AC
 DT 28-JAN-1997 (first entry)
 XX
 DE Human MDM-2 gene cDNA clone, involved in tumour-development.
 XX
 KW p53; MDM-2; binding-inhibitor; identification; tumour; cancer;
 XX neoplasia; antibody fusion protein; therapy; ds.
 OS Homo sapiens.
 FH Key
 CDS 312..1787
 FT /*tag= a
 XX
 PN US5550023-A.
 XX
 PD 27-AUG-1996.
 XX
 PF 07-APR-1992; 92US-0867840.
 XX
 PR 07-APR-1993; 93US-0044619.
 PR 07-APR-1992; 92US-0867840.
 PR 23-JUN-1992; 92US-0903103.
 PR 18-MAY-1994; 94US-0245500.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Kinzler KW, Vogelstein B;
 XX

| | | | |
|-----------|--|--|------|
| Db | 1801 | AAGAGAAATTATATATTTCCTAACTATATATAACCTCGAATTTAGACAACTGAAATTTATT | 1860 |
| Qy | 1861 | CACATATATCAAAGTGGAGAAATGCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT | 1920 |
| Db | 1861 | CACATATATCAAAGTGGAGAAATGCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT | 1920 |
| Qy | 1921 | TGACCTACTTTGGTAGTGGAAATGAGTACATTTACTATAATTTGACTTGAATATGTAGCT | 1980 |
| Db | 1921 | TGACCTACTTTGGTAGTGGAAATGAGTACATTTACTATAATTTGACTTGAATATGTAGCT | 1980 |
| Qy | 1981 | CATCCTTTACACCAACTCCCTAAATTTTAAATATTTTCTACTCTGTCTTAAATGAGAACTAC | 2040 |
| Db | 1981 | CATCCTTTACACCAACTCCCTAAATTTTAAATATTTTCTACTCTGTCTTAAATGAGAACTAC | 2040 |
| Qy | 2041 | TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTAATTTTCTTTT | 2100 |
| Db | 2041 | TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTAATTTTCTTTT | 2100 |
| Qy | 2101 | AGACCGAGTCTTGCTCTGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTTGGCTCAGCTGCA | 2160 |
| Db | 2101 | AGACCGAGTCTTGCTCTGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTTGGCTCAGCTGCA | 2160 |
| Qy | 2161 | AGCTCTGCCCTCCCGGGTTGCCACCATTTCTCCTGCCTCAGCTCCCAATAGCTTGGCC | 2220 |
| Db | 2161 | AGCTCTGCCCTCCCGGGTTGCCACCATTTCTCCTGCCTCAGCTCCCAATAGCTTGGCC | 2220 |
| Qy | 2221 | TACAGTCTATCGCCACACACACCTGGCTAAATTTTGTACTTTTGTAGAGACAGGGTTTC | 2280 |
| Db | 2221 | TACAGTCTATCGCCACACACACCTGGCTAAATTTTGTACTTTTGTAGAGACAGGGTTTC | 2280 |
| Qy | 2281 | ACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGCGCTCC | 2340 |
| Db | 2281 | ACCGTGTAGCCAGGATGGTCTCGATCTCCTGACCTCGTATCCGCCACCTCGCGCTCC | 2340 |
| Qy | 2341 | CAAAAGTCTGGGATTACAGGCATGAGCCACCG | 2372 |
| Db | 2341 | CAAAAGTCTGGGATTACAGGCATGAGCCACCG | 2372 |
| RESULT 5 | | | |
| AAAT62065 | | | |
| ID | AAAT62065 standard; cDNA; 2372 bp. | | |
| XX | AAAT62065; | | |
| AC | | | |
| DT | 05-JUN-1997 (first entry) | | |
| XX | Human MDM2 cDNA. | | |
| DE | | | |
| XX | Human; MDM2; CaCo-2; colonic; carcinoma; probe; detection; | | |
| KW | amplification; elevation; expression; diagnosis; neoplasia; | | |
| KW | neoplastic transformation; sarcoma; colorectal; lung cancer; | | |
| KW | chronic myelogenous leukaemia; ds. | | |
| XX | | | |
| OS | Homo sapiens. | | |
| XX | | | |
| FH | Key | Location/Qualifiers | |
| FT | CDS | 312..1787 | |
| FT | | /*tag= a | |
| FT | | /product= MDM2 | |
| XX | | | |
| PN | US5606044-A. | | |
| PD | | | |
| XX | 25-FEB-1997. | | |
| XX | | | |
| PF | 07-APR-1992; | 92US-0867840. | |
| XX | | | |
| PR | 07-APR-1993; | 93US-0044619. | |
| PR | 07-APR-1992; | 92US-0867840. | |
| PR | 23-JUN-1992; | 92US-0903103. | |
| PR | 17-FEB-1995; | 95US-0390546. | |
| XX | | | |

QY 1801 AAGAGATTATATATTTCTAAGTATATATACCTAGGAATTTAGACAACTGAAATTTATT 1860
 Db 1801 AAGAGATTATATATTTCTAAGTATATATACCTAGGAATTTAGACAACTGAAATTTATT 1860
 QY 1861 CACATATATCAAAAGTGGAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
 Db 1861 CACATATATCAAAAGTGGAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
 QY 1921 TGACCTACTTTGGTAGTGAATAGTGAATAGTGAATAGTGAATAGTGAATAGTGAAT 1980
 Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATAGTGAATAGTGAATAGTGAATAGTGAAT 1980
 QY 1981 CATCTTTTACACCAACTCCTAAATTTTAAATAATTTCTACTCTGTCTTAAATGAGAATAC 2040
 Db 1981 CATCTTTTACACCAACTCCTAAATTTTAAATAATTTCTACTCTGTCTTAAATGAGAATAC 2040
 QY 2041 TTGGTATTTTCTTAAATAGTATAGATTTAAATGATTAATGATTAATGATTAATGATTA 2100
 Db 2041 TTGGTATTTTCTTAAATAGTATAGATTTAAATGATTAATGATTAATGATTAATGATTA 2100
 QY 2101 AGACCGAGTCTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGCTCACTGCA 2160
 QY 2161 AGCTCTGCCCTCCCGGGTTCGACCATCTCTGCTCAGCTCCCAATTAGCTTGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTCGACCATCTCTGCTCAGCTCCCAATTAGCTTGCC 2220
 QY 2221 TACAGTCTGCCACACACCTGGCTAAATTTTGTACTTTAGTAGACAGGGTTTC 2280
 Db 2221 TACAGTCTGCCACACACCTGGCTAAATTTTGTACTTTAGTAGACAGGGTTTC 2280
 QY 2281 ACCGTGTAGCAGGATGTCGATCTCTGACCTCTGATCCGCCACCTCCGCTCCGCTCC 2340
 Db 2281 ACCGTGTAGCAGGATGTCGATCTCTGACCTCTGATCCGCCACCTCCGCTCCGCTCC 2340
 QY 2341 CAAAGTCTGGGATTACAGCATGAGCCACG 2372
 Db 2341 CAAAGTCTGGGATTACAGCATGAGCCACG 2372

RESULT 6
 AAV28876
 ID AAV28876 standard; cDNA; 2372 BP.
 XX
 AC AAV28876;
 XX
 DE Human MDM2 gene.
 XX
 KW Human; p53; MDM2; tumour; growth inhibition; amplification;
 KW malignant fibrous histiocytoma; liposarcoma; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 312..1787
 FT /*tag= a
 FT /product= "MDM2 protein"
 XX
 PN US5756455-A,
 XX
 PD 26-MAY-1998.
 XX
 PF 17-FEB-1995; 9505-0390515.
 XX
 PR 07-APR-1993; 9305-004619.
 PR 07-APR-1992; 9205-0867840.
 PR 23-JUN-1992; 9205-0903103.
 PR 17-FEB-1995; 9505-0390515.
 XX

(UYJO) UNIV JOHNS HOPKINS.
 XX Kinzler KW, Vogelstein B;
 XX WPI; 1998-321574/28.
 DR P-PSDB; AAW57241.
 XX Inhibiting growth of tumour cells having MDM2 gene amplification -
 PT with p53 protein fragment
 XX
 XX Example 1; Column 19-24; 40pp; English.
 XX
 PS A method has been developed for inhibiting the growth of tumour cells
 CC containing a human MDM2 gene amplification. The method comprises
 CC treating the tumour cells with a DNA molecule that expresses a
 CC polypeptide capable of binding to human MDM2 protein. The present
 CC sequence represents the human MDM2 gene. The present invention describes
 CC three preferred polypeptides for binding human MDM2: (1) the polypeptide
 CC comprises amino acids 1-50 of p53 (see AAW57240); (2) the polypeptide
 CC comprises amino acids 13-41 of p53 (see AAW57240) and at least none
 CC additional p53 residues on the N- or C-terminal side, provided that the
 CC polypeptide lacks the homooligomerisation domain of p53; (3) the
 CC polypeptide comprises amino acids 13-41 of p53 (see AAW57241) and at
 CC least nine additional p53 residues on the N- or C-terminal side, provided
 CC that the polypeptide lacks amino acids 138-393 of p53. Some malignant
 CC fibrous histiocytomas and liposarcomas have an MDM2 gene amplification,
 CC so detection of increased expression of MDM2 gene products indicates
 CC tumorigenesis.
 XX
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
 XX
 Query Match 100.0%; Score 2372; DB 19; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCACCGCGGAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 Db 1 GCACCGCGGAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 QY 61 GCAAGAGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 Db 61 GCAAGAGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
 QY 121 CAGCCAGGACGACCGCTCCCTCCCGGATAGTGGTACGAGCGGCGGCGGCGGCGGCGG 180
 Db 121 CAGCCAGGACGACCGCTCCCTCCCGGATAGTGGTACGAGCGGCGGCGGCGGCGGCGG 180
 QY 181 GAGAGTGAATGATCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 Db 181 GAGAGTGAATGATCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
 QY 241 AAGGAACTGGGAGTCTTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 Db 241 AAGGAACTGGGAGTCTTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 QY 301 GGAGCGCAAAATGTGCAATACCAACATGTCTGTACTACTGTGTGTGTGTGTGTGTGT 360
 Db 301 GGAGCGCAAAATGTGCAATACCAACATGTCTGTACTACTGTGTGTGTGTGTGTGTGT 360
 QY 361 CACAGATTCCAGCTTCGGAACAGAGACCGCTGGTTAGACCAAGCCATTGCTTTGAAGT 420
 Db 361 CACAGATTCCAGCTTCGGAACAGAGACCGCTGGTTAGACCAAGCCATTGCTTTGAAGT 420
 QY 421 TATTAAGTCTGTGGTGCACAAAAGACACTTATATGATGAGAGGTTCTTTTATC 480
 Db 421 TATTAAGTCTGTGGTGCACAAAAGACACTTATATGATGAGAGGTTCTTTTATC 480
 QY 481 TTGGCCAGTATATTATGACTAAACGATTTATGATGAGAGCAACACATATTGTATATT 540
 Db 481 TTGGCCAGTATATTATGACTAAACGATTTATGATGAGAGCAACACATATTGTATATT 540
 QY 541 GTTCAATGATCTTCTAGGAGATTGTTGGGCGTCCCAAGCTTCTCTGTGAAAGACACA 600
 Db 541 GTTCAATGATCTTCTAGGAGATTGTTGGGCGTCCCAAGCTTCTCTGTGAAAGACACA 600

Db 541 GTTCAATGATCTTCTAGGAGATTGTTGGCGTGCCAGCTTCTCTGTGAAAGACACA 600
QY 601 CGAAATATATACCATGATCTACAGGAACCTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
Db 601 CGAAATATATACCATGATCTACAGGAACCTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
QY 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTCACTTGAAGTGGAGTGATCAAAAGG 720
Db 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTCACTTGAAGTGGAGTGATCAAAAGG 720
QY 721 ACCTTGTAACAGAGCTTCAGGAAGAGAACTTCATCTTCACATTTGGTTCTAGACCAT 780
Db 721 ACCTTGTAACAGAGCTTCAGGAAGAGAACTTCATCTTCACATTTGGTTCTAGACCAT 780
QY 781 CTACCTCATCTAGAGAGAGACCAATTAGTGAGACAGAGAAGAAATTCAGATGAATATCTG 840
Db 781 CTACCTCATCTAGAGAGAGACCAATTAGTGAGACAGAGAAGAAATTCAGATGAATATCTG 840
QY 841 GTGAACGCAAAAGAAAGCCACAAATCTGATAGTATTTCCCTTTCCTTTGATGAAGCC 900
Db 841 GTGAACGCAAAAGAAAGCCACAAATCTGATAGTATTTCCCTTTCCTTTGATGAAGCC 900
QY 901 TGGCTCTGTGTATATAGGAGAGATATGTGTGAAGAACAGCAGTACAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTATATAGGAGAGATATGTGTGAAGAACAGCAGTACAGTGAATCTACAG 960
QY 961 GGACGCCATCGAATCCGGATCTTGATGCTGTGTGAAGTGAACATTCAGGTGATGGTTGG 1020
Db 961 GGACGCCATCGAATCCGGATCTTGATGCTGTGTGAAGTGAACATTCAGGTGATGGTTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGNATTTGAAGTTGAATCTCTCGACTCAG 1080
Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGNATTTGAAGTTGAATCTCTCGACTCAG 1080
QY 1081 AAGATTATAGCCTTAGTGAAGAGGACAAAGAACTCTCAGATGAAGTATGAGGTATATC 1140
Db 1081 AAGATTATAGCCTTAGTGAAGAGGACAAAGAACTCTCAGATGAAGTATGAGGTATATC 1140
QY 1141 AAGTTACTGTGTATCAGCAGGGAGAGTGTATCAGATTCATTTGAAGAGATCTCTGAAA 1200
Db 1141 AAGTTACTGTGTATCAGCAGGGAGAGTGTATCAGATTCATTTGAAGAGATCTCTGAAA 1200
QY 1201 TTTCCTTAGCTATTTGGAATGCACTTCATGCAATGAATGAATCCGCCCTTCCAT 1260
Db 1201 TTTCCTTAGCTATTTGGAATGCACTTCATGCAATGAATGAATCCGCCCTTCCAT 1260
QY 1261 CACATGCAACAGATTTGGCCCTTCTGAGATTTGGCTTCCTGAGATTAAGAGGAAG 1320
Db 1261 CACATGCAACAGATTTGGCCCTTCTGAGATTTGGCTTCCTGAGATTAAGAGGAAG 1320
QY 1321 ATAAAGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAGCTGAAGAGGCT 1380
Db 1321 ATAAAGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAGCTGAAGAGGCT 1380
QY 1381 TTGATGTTCTCATTTAAAGAACTATAGTGAATGATCCAGAGATCATGTGTTGAGG 1440
Db 1381 TTGATGTTCTCATTTAAAGAACTATAGTGAATGATCCAGAGATCATGTGTTGAGG 1440
QY 1441 AAATGATGATAAAATACAAAGCTTCACAAATCACAAGAAAGTGAAGATATTTCTCAGC 1500
Db 1441 AAATGATGATAAAATACAAAGCTTCACAAATCACAAGAAAGTGAAGATATTTCTCAGC 1500
QY 1501 CATCACTCTAGTAGCATTTATATAGCAGCCAGAGATGTCAGAGATTCAGAGGTTGAAGG 1560
Db 1501 CATCACTCTAGTAGCATTTATATAGCAGCCAGAGATGTCAGAGATTCAGAGGTTGAAGG 1560
QY 1561 AAGAAACCCAGCAAAAGAGAGTGTGGAATCTAGTTTCCCTTAAATGCAATTTGAAC 1620
Db 1561 AAGAAACCCAGCAAAAGAGAGTGTGGAATCTAGTTTCCCTTAAATGCAATTTGAAC 1620
QY 1621 CTTGTGTGATTTGTCAGGTGCACTTAAATGCTTCCATTTCCATGCGCAAAACAGGAC 1680
Db 1621 CTTGTGTGATTTGTCAGGTGCACTTAAATGCTTCCATTTCCATGCGCAAAACAGGAC 1680

QY 1681 ATCTATGGCGCTTTACATGTCAAAAGAGCTAAAGAAAGAAATAGCCCTGCCCCAG 1740
Db 1681 ATCTATGGCGCTTTACATGTCAAAAGAGCTAAAGAAAGAAATAGCCCTGCCCCAG 1740
QY 1741 TATGTAGACAACCAATTCAAATGATTGCTAACTTATTTCCCTAGTTGACCTGCTAT 1800
Db 1741 TATGTAGACAACCAATTCAAATGATTGCTAACTTATTTCCCTAGTTGACCTGCTAT 1800
QY 1801 AAGAGAAATATATATTTCTTAACATATATAACCCCTAGGAATTTAGACAACCTCAAAATTA 1860
Db 1801 AAGAGAAATATATATTTCTTAACATATATAACCCCTAGGAATTTAGACAACCTCAAAATTA 1860
QY 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
Db 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
QY 1921 TGACCTACTTTGGTAGTGAATAGTAACTACTTACTATAATTTGACTTGAATATGTAGCT 1980
Db 1921 TGACCTACTTTGGTAGTGAATAGTAACTACTTACTATAATTTGACTTGAATATGTAGCT 1980
QY 1981 CATCCTTTACCAACTCTTAATTTAAATTAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
Db 1981 CATCCTTTACCAACTCTTAATTTAAATTAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
QY 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATTAATTTTATTTT 2100
Db 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATTAATTTTATTTT 2100
QY 2101 AGACCCAGCTGTCTCTGTACCCAGGCTGGAGTGCAGTGGTGCATCTTGCTCAGCTGCA 2160
Db 2101 AGACCCAGCTGTCTCTGTACCCAGGCTGGAGTGCAGTGGTGCATCTTGCTCAGCTGCA 2160
QY 2161 AGCTCTGCTCCCGGGTTCGCACCATTTCTCTGCTCAGCTCCCAATTAGCTTGCC 2220
Db 2161 AGCTCTGCTCCCGGGTTCGCACCATTTCTCTGCTCAGCTCCCAATTAGCTTGCC 2220
QY 2221 TACAGTCACTGCCCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGGGTTTC 2280
Db 2221 TACAGTCACTGCCCACACACCTGGCTAATTTTGTACTTTTAGTAGACAGGGTTTC 2280
QY 2281 ACCGTGTTAGCCAGGATGCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCCTC 2340
Db 2281 ACCGTGTTAGCCAGGATGCTCGATCTCTGATCTCTGATCCGCCACCTCGGCCCTC 2340
QY 2341 CAAAGTCTGGGATTCAGCATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTCAGCATGAGCCACCG 2372

RESULT 7

AAV20549
ID AAV20549 standard; cdna; 2372 BP.

XX

XX AAV20549;

XX AC

XX 18-JUN-1998 (first entry)

XX DF

XX Human MD2 encoding cdna.

XX DE

XX KW Human; MD2; hMD2; tumour; cancer; diagnosis; neoplastic disease;
sarcoma; liposarcoma; malignant fibrous histiocyoma; osteosarcoma; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 312..1787

XX FT /*tag= a

XX FT /product= "MD2"

XX XX

XX US5736338-A.

XX PN

XX 07-APR-1998.

XX PD

XX PF 17-FEB-1995; 95US-0390517.
XX PR 07-APR-1993; 93US-0044619.
XX PR 07-APR-1992; 92US-0867840.
XX PR 23-JUN-1992; 92US-0903103.
XX PR 17-FEB-1995; 95US-0390517.
XX PA (UVOJ) UNIV JOHNS HOPKINS.
XX PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;
XX DR WPI; 1998-239206/21.
XX DR P-PSDB; AAW48241.
XX PT Cancer diagnosis - by determination of MDM2 protein
XX PS Claim 1; Column 21-24; 35pp; English.
XX CC The present sequence encodes human MDM2 (hMDM2) which is used in the
CC method of the present invention. The present invention describes a
CC method for diagnosing a neoplastic disease caused by overexpression
CC of MDM2 protein. The method comprises detecting an elevated cellular
CC amount of this protein. The method is useful for the diagnosis of
CC sarcoma, especially liposarcoma, malignant fibrous histiocytoma or
CC osteosarcoma.
XX CC
XX SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
Query Match 100.0%; Score 2372; DB 19; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCGCGGAGCTTGGCTGCTCTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
DB 1 GCACCGCGGAGCTTGGCTGCTCTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
QY 61 GCAGAAGCGGCGCGGAGGGGCGCGGACCCCTCTGACGGAGATCTGCTGCTTTCG 120
DB 61 GCAAGAAGCGGCGGAGGGGCGCGGACCCCTCTGACGGAGATCTGCTGCTTTCG 120
QY 121 CAGCAGGAGCAGCGCTCCCTCCCGGATTAGTGCCTAGGAGCGCCGCTGCGCTTTCG 180
DB 121 CAGCAGGAGCAGCGCTCCCTCCCGGATTAGTGCCTAGGAGCGCCGCTGCGCTTTCG 180
QY 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGCTTCCGAGTAGTCACTCCCGTG 240
DB 181 GAGAGTGAATGATCCCGAGGCGCCAGGCGCTGCTTCCGAGTAGTCACTCCCGTG 240
QY 241 AAGGAAACTGGGAGTCTTGGAGGACCCCGGACTCCAGCGCGAAACCCCGGATGTGA 300
DB 241 AAGGAAACTGGGAGTCTTGGAGGACCCCGGACTCCAGCGCGAAACCCCGGATGTGA 300
QY 301 GGAGCAGCAATGTGCAATACCAATCTGTACTCTGTACTGTGCTGTACCACT 360
DB 301 GGAGCAGCAATGTGCAATACCAATCTGTACTCTGTACTGTGCTGTACCACT 360
QY 361 CACAGATTCAGGCTTCGGAACAGAGACCCCTGTTAGACCAAGCCATTCCTTTGAAGT 420
DB 361 CACAGATTCAGGCTTCGGAACAGAGACCCCTGTTAGACCAAGCCATTCCTTTGAAGT 420
QY 421 TATTAAAGTCTGTTGGTGCAAAAAGACACTTATATCTATGAAAGAGTCTTTTATC 480
DB 421 TATTAAAGTCTGTTGGTGCAAAAAGACACTTATATCTATGAAAGAGTCTTTTATC 480
QY 481 TTGGCCAGTATATATGACTAAACGATTATATGATGAGAAGCAACATATTGTATTT 540
DB 481 TTGGCCAGTATATATGACTAAACGATTATATGATGAGAAGCAACATATTGTATTT 540
QY 541 GTTCAAAATGATCTCTAGGAGATTCTTTGGCGTGCAGCTTCTCTGTGAAGAGCACA 600
DB 541 GTTCAAAATGATCTCTAGGAGATTCTTTGGCGTGCAGCTTCTCTGTGAAGAGCACA 600

QY 601 GGAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGCAATCATCGG 660
DB 601 GGAAATATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGCAATCATCGG 660
QY 661 ACTCAGGTACATCTGTGAGTGAGAACAGGCTACCTTTGAAGGTGGGAGTGATCAAAAG 720
DB 661 ACTCAGGTACATCTGTGAGTGAGAACAGGCTACCTTTGAAGGTGGGAGTGATCAAAAG 720
QY 721 ACCTTGTACAGAGCTTTCAGGAGAGAACCTTCACTTTCATTTGCTTCTTCTAGACCAT 780
DB 721 ACCTTGTACAGAGCTTTCAGGAGAGAACCTTCACTTTCATTTGCTTCTTCTAGACCAT 780
QY 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATTTCTG 840
DB 781 CTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATTTCTG 840
QY 841 GTGAACGACAAAGAAACGCCACAATCTGATAGTATTTCCCTTTCCTTTGATGAAAGCC 900
DB 841 GTGAACGACAAAGAAACGCCACAATCTGATAGTATTTCCCTTTCCTTTGATGAAAGCC 900
QY 901 TGGCTCTGTGTGTAATAGGGAGATATTTGTGAAAGAGCAGTAGCAGTGAATTTCTACAG 960
DB 901 TGGCTCTGTGTGTAATAGGGAGATATTTGTGAAAGAGCAGTAGCAGTGAATTTCTACAG 960
QY 961 GGAGCCATCGAATCCGGATCTTGATGCTGTGTGTAAGTGAACATTCAGGTGATTGTTGG 1020
DB 961 GGAGCCATCGAATCCGGATCTTGATGCTGTGTGTAAGTGAACATTCAGGTGATTGTTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAAAGTTGATCTCTGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAAAGTTGATCTCTGACTCAG 1080
QY 1081 AAGATTATACCTTAGTGAAGAGGACAAAGAACTCTCAGATGAAGATGATGAGTATATC 1140
DB 1081 AAGATTATACCTTAGTGAAGAGGACAAAGAACTCTCAGATGAAGATGATGAGTATATC 1140
QY 1141 AAGTTACTGTGTATCAGGAGGAGAGTATACAGATTCATTTGAAGAGATCCTGAAA 1200
DB 1141 AAGTTACTGTGTATCAGGAGGAGAGTATACAGATTCATTTGAAGAGATCCTGAAA 1200
QY 1201 TTTCTTTAGTCTACTATTTGSAATGCACTTCATGCAATGAAATGAATCCCTCCCTTCCAT 1260
DB 1201 TTTCTTTAGTCTACTATTTGSAATGCACTTCATGCAATGAAATGAATCCCTCCCTTCCAT 1260
QY 1261 CACATTCGACACAGATCTTGGCCCTTCGTGAGAAATGAGTTCCTCCTCAAGATAAAGGAAAG 1320
DB 1261 CACATTCGACACAGATCTTGGCCCTTCGTGAGAAATGAGTTCCTCCTCAAGATAAAGGAAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAGCTGAAGAGGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAGCTGAAGAGGGCT 1380
QY 1381 TTGATGTTCTGATTTGTAATAAAGTATAGTCAATGATTCAGAGAGTCACTGTTGAGG 1440
DB 1381 TTGATGTTCTGATTTGTAATAAAGTATAGTCAATGATTCAGAGAGTCACTGTTGAGG 1440
QY 1441 AAAATGATGATAAAATTCACAAAGCTTCAATCAACAAGAAAGTGAAGACTATTCTCAGC 1500
DB 1441 AAAATGATGATAAAATTCACAAAGCTTCAATCAACAAGAAAGTGAAGACTATTCTCAGC 1500
QY 1501 CATCAACTTCTAGTAGCATTTATTTATAGCAGCCAAAGAGATGTGAAGAGTTTCAAGGG 1560
DB 1501 CATCAACTTCTAGTAGCATTTATTTATAGCAGCCAAAGAGATGTGAAGAGTTTCAAGGG 1560
QY 1561 AAGAAACCCAGACAAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAAATGCCATTTGAAC 1620
DB 1561 AAGAAACCCAGACAAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAAATGCCATTTGAAC 1620
QY 1621 CTTCTGTGATTGTGAAGTCCAGCTTAAATTTGTTGATTTGCCATTCCTGCAAAACAGGAC 1680
DB 1621 CTTCTGTGATTGTGAAGTCCAGCTTAAATTTGTTGATTTGCCATTCCTGCAAAACAGGAC 1680
QY 1681 ATCTTATGGCCCTGCTTTACATGTGCAAGAGACTAAAGAAAGGAAATTAAGCCCTGCCAG 1740

1681 ATCTTATGCGCTGCTTTACATGTGCAAGAGCTTAAAGAAAGAAATAAGCCCTGCCCCAG 1740
 1741 TATGTAGACCAACCAATCAAAATGATGTGCTTAACCTTATTTCCCTAGTTGACCTGCTAT 1800
 1741 TATGTAGACCAACCAATCAAAATGATGTGCTTAACCTTATTTCCCTAGTTGACCTGCTAT 1800
 1801 AAGAGAAATATATATTTCTAACTATATAACCCCTAGGAATTTAGACAACTGAAATTTAT 1860
 1801 AAGAGAAATATATATTTCTAACTATATAACCCCTAGGAATTTAGACAACTGAAATTTAT 1860
 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAT 1920
 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAT 1920
 1921 TGACCTACTTTGGTGTAGTGGAAATAGTAATCTTACTATAATTTGACTTGAATGTAGCT 1980
 1921 TGACCTACTTTGGTGTAGTGGAAATAGTAATCTTACTATAATTTGACTTGAATGTAGCT 1980
 1981 CATCCTTTACCAACCACTCTTAATTTTAAATTAATTTCTACTCTGTCTTAATGAGAAGTAC 2040
 1981 CATCCTTTACCAACCACTCTTAATTTTAAATTAATTTCTACTCTGTCTTAATGAGAAGTAC 2040
 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTATTTATTTTGTG 2100
 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTATTTATTTTGTG 2100
 2101 AGACCGAGTCTTGTCTGTACCCAGGCTGGAGTGCAGTGGCTGATCTTGGCTCACTGCA 2160
 2101 AGACCGAGTCTTGTCTGTACCCAGGCTGGAGTGCAGTGGCTGATCTTGGCTCACTGCA 2160
 2161 AGCTCTGCGCCTCCCGGGTTCGACCAATCTCTGCTGACCTTCCCAATTTAGCTTGGCC 2220
 2161 AGCTCTGCGCCTCCCGGGTTCGACCAATCTCTGCTGACCTTCCCAATTTAGCTTGGCC 2220
 2221 TACAGTCATCTGCCACCACTGCTGCTAATTTTGTACTTTTGTAGTACACAGGCTTTC 2280
 2221 TACAGTCATCTGCCACCACTGCTGCTAATTTTGTACTTTTGTAGTACACAGGCTTTC 2280
 2281 ACCGTGTTAGCAGATGCTGCTGATCTGCTGACCTTCCGATCGCCGCTCGGCTCC 2340
 2281 ACCGTGTTAGCAGATGCTGCTGATCTGCTGACCTTCCGATCGCCGCTCGGCTCC 2340
 2341 CAAAGTCTGGGATACAGGATGAGCCACCG 2372
 2341 CAAAGTCTGGGATACAGGATGAGCCACCG 2372

RESULT 8
 AAV04836
 ID AAV04836 standard; cDNA; 2372 BP.

AC AAV04836;
 AC AAV04836;
 DT 30-APR-1998 (first entry)
 XX cDNA sequence of human MDM2.

DE MDM2; tumour; diagnosis; neoplasia; DNA binding protein;
 KW p53 polypeptide; binding; tumour cell; p53-regulated growth;
 KW inhibition; anti-cancer agent; ds.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 312..1787
 FT CDS /*tag= a

XX US5708136-A.
 XX 13-JAN-1998.
 XX 17-FEB-1995; 9505-0390516.

XX 07-APR-1993; 93US-0044619.
 PR 07-APR-1992; 92US-0867840.
 PR 23-JUN-1992; 92US-0903103.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Burrell M, Hill DE, Kinzler KW, Vogelstein B;
 PI MPI; 1998-100408/09.
 XX Human MDM2 binding polypeptide - comprises fragments of p53, useful
 in re-establishing p53-regulated growth control in cells
 over-expressing MDM2
 Disclosure; Columns 19-24; 41pp; English.
 XX The present sequence encodes human MDM2. The MDM2 gene is amplified in
 some human tumours. The amplification of this gene is diagnostic of
 neoplasia or its potential. It is speculated that the MDM2 protein is a
 potential DNA binding protein that functions in the modulation of
 expression of other genes and, when present in excess, interferes with
 normal constraints on cell growth. A cell containing three recombinant
 DNA constructs was produced. These constructs encode an MDM2 protein
 fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
 to a transcriptional activation domain, and a reporter gene downstream
 from a DNA element which is recognised by the sequence-specific
 DNA-binding domain. The cell is used to identify a compound which
 interferes with the binding of MDM2 and p53. Since MDM2 is overexpressed
 in tumour cells and since binding of MDM2 to p53 appears to allow tumour
 cells to escape from p53-regulated growth, compounds that inhibit such
 binding would be useful as anti-cancer agents.
 XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;
 Query Match 100.0%; Score 2372; DB 19; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 DB 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 QY 61 GCAAGAACCGCAGCGCGGCGCGCGCCCTCTGACCGAGATCCTGCTGCTTTTCG 120
 DB 61 GCAAGAACCGCAGCGCGGCGCGCCCTCTGACCGAGATCCTGCTGCTTTTCG 120
 QY 121 CAGCCAGGACACCTGCTCCCTCCCGGATTTAGTGTAGAGGCGCCAGTGGCCCTGGCCCG 180
 DB 121 CAGCCAGGACACCTGCTCCCTCCCGGATTTAGTGTAGAGGCGCCAGTGGCCCTGGCCCG 180
 QY 181 GAGAGTGAATGATCCCGCAGGCGCGCTGCTGCTTCCGAGTGTAGTCACTCCCGCTG 240
 DB 181 GAGAGTGAATGATCCCGCAGGCGCGCTGCTGCTTCCGAGTGTAGTCACTCCCGCTG 240
 QY 241 AAGGAACTGGGAGTCTTGGAGGACCCCGGACTCCAGCGGAAACCCCGGATGTGA 300
 DB 241 AAGGAACTGGGAGTCTTGGAGGACCCCGGACTCCAGCGGAAACCCCGGATGTGA 300
 QY 301 GGAGCAGGCAAAATGTGCAATATACCAATGCTGTACTACTGATGCTGCTGTAAACCACT 360
 DB 301 GGAGCAGGCAAAATGTGCAATATACCAATGCTGTACTACTGATGCTGCTGTAAACCACT 360
 QY 361 CACAGATTCAGCTTCGGAAACAGAGACCTGTTAGACCAAGCCATTTGTTTGAAGT 420
 DB 361 CACAGATTCAGCTTCGGAAACAGAGACCTGTTAGACCAAGCCATTTGTTTGAAGT 420
 QY 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATACTATGAAGAGGTTCTTTTATC 480
 DB 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATACTATGAAGAGGTTCTTTTATC 480
 QY 481 TTGCCAGTATATTTGACTAAACGATTATATGATGAGACGACACATATTTGTATATT 540
 DB 481 TTGCCAGTATATTTGACTAAACGATTATATGATGAGACGACACATATTTGTATATT 540

Db 481 TTGCCAGTATATATGACTAAACGATATATGATGAGAGCAACAAATATTGTATATT 540
 Qy 541 GTTCAAAATGATCTTCTAGGAGATTTGTTGGCGTGCACAGCTTCTCTGTGAAGAGCACA 600
 Db 541 GTTCAAAATGATCTTCTAGGAGATTTGTTGGCGTGCACAGCTTCTCTGTGAAGAGCACA 600
 Qy 601 GGAATAATATACCATGATCTACAGNACTTGTAGTAGTCATCAGCAGGAATCATCGG 560
 Db 601 GGAATAATATACCATGATCTACAGNACTTGTAGTAGTCATCAGCAGGAATCATCGG 560
 Qy 661 ACTCAGGTACATCTGTGAGTGAGAGAGAGTGTCAACCTTGAAGGTGGAGTGTCAAAAGG 720
 Db 661 ACTCAGGTACATCTGTGAGTGAGAGAGAGTGTCAACCTTGAAGGTGGAGTGTCAAAAGG 720
 Qy 721 ACCTTGTACAGAGCTTTCAGAGAGAGAACTTCATCTTCACATTTGGTTTCTAGACCAAT 780
 Db 721 ACCTTGTACAGAGCTTTCAGAGAGAGAACTTCATCTTCACATTTGGTTTCTAGACCAAT 780
 Qy 781 CTACCTCATCTAGAGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATTTATCTG 840
 Db 781 CTACCTCATCTAGAGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATTTATCTG 840
 Qy 841 GTGACGCAAGAAACGCCACAATCTGATAGTATTTCCCTTTCCTTTGATGAAGGC 900
 Db 841 GTGACGCAAGAAACGCCACAATCTGATAGTATTTCCCTTTCCTTTGATGAAGGC 900
 Qy 901 TGGCTCTGTGTATTAAGGAGATATGTTGTAAGAGCAGTACAGTGAATCTACAG 960
 Db 901 TGGCTCTGTGTATTAAGGAGATATGTTGTAAGAGCAGTACAGTGAATCTACAG 960
 Qy 961 GGAGCCCATCAATCCGGATCTTGATGCTGGTGTAGTGAACATTCAGGTGATTTGGTGG 1020
 Db 961 GGAGCCCATCAATCCGGATCTTGATGCTGGTGTAGTGAACATTCAGGTGATTTGGTGG 1020
 Qy 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAATTTGATCTCTCAGCTCAG 1080
 Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAATTTGATCTCTCAGCTCAG 1080
 Qy 1081 AAGATTATAGCCTTATGGAAGAGGACAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
 Db 1081 AAGATTATAGCCTTATGGAAGAGGACAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
 Qy 1141 AAGTTACTGTCTATCAGCAGGAGAGTATACAGATTCATTTGAAGAGATCTGAA 1200
 Db 1141 AAGTTACTGTCTATCAGCAGGAGAGTATACAGATTCATTTGAAGAGATCTGAA 1200
 Qy 1201 TTTCCCTTAGCTGACTTATGGAATGCACTTCATGCAATGAATGNAATCCCTCCCTTCCAT 1260
 Db 1201 TTTCCCTTAGCTGACTTATGGAATGCACTTCATGCAATGAATGNAATCCCTCCCTTCCAT 1260
 Qy 1261 CACATTGCAACAGATGTTGGCCCTTCGTGAGATTTGGCTTCCTGAGATTAAGGGAAG 1320
 Db 1261 CACATTGCAACAGATGTTGGCCCTTCGTGAGATTTGGCTTCCTGAGATTAAGGGAAG 1320
 Qy 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAAGAACTCAACACAGCTGAAGAGGGCT 1380
 Db 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAAGAACTCAACACAGCTGAAGAGGGCT 1380
 Qy 1381 TTGATGTTCCCTGATGTAAGAAATATAGTGAATGATTCAGAGAGTCAATGTTGAGG 1440
 Db 1381 TTGATGTTCCCTGATGTAAGAAATATAGTGAATGATTCAGAGAGTCAATGTTGAGG 1440
 Qy 1441 AAAATGATGATAAATACACAAGCTTCACAAATCACAAGAAAGTGAAGACTATTCTCAGC 1500
 Db 1441 AAAATGATGATAAATACACAAGCTTCACAAATCACAAGAAAGTGAAGACTATTCTCAGC 1500
 Qy 1501 CATCAACTCTAGTAGCATATTATATAGCAGCAGAGATGGAAGAGTTTGAAGGG 1560
 Db 1501 CATCAACTCTAGTAGCATATTATATAGCAGCAGAGATGGAAGAGTTTGAAGGG 1560
 Qy 1561 AAGAACAACCAAGACAAAGAGAGTGTGGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
 Db 1561 AAGAACAACCAAGACAAAGAGAGTGTGGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620

Qy 1621 CTTGTGTGATTTGTCAAGGTGACCTAAAAATGGTTGCAATGTGTCATGAGCAAAACAGGAC 1680
 Db 1621 CTTGTGTGATTTGTCAAGGTGACCTAAAAATGGTTGCAATGTGTCATGAGCAAAACAGGAC 1680
 Qy 1681 ATCTTATGGCCTGCTTTACATGTGCAAGAGCTAAAGAAAAGGATAAGCCCTGCCAG 1740
 Db 1681 ATCTTATGGCCTGCTTTACATGTGCAAGAGCTAAAGAAAAGGATAAGCCCTGCCAG 1740
 Qy 1741 TATGTAGACAACCAATTCAAATGATTGTGCTAACTATTATTTCCCTAGTGTGCTAT 1800
 Db 1741 TATGTAGACAACCAATTCAAATGATTGTGCTAACTATTATTTCCCTAGTGTGCTAT 1800
 Qy 1801 AAGAGATATATATTTCTAACTATATAACCTTAGGAATTTAGACAACTGAAATTTAT 1860
 Db 1801 AAGAGATATATATTTCTAACTATATAACCTTAGGAATTTAGACAACTGAAATTTAT 1860
 Qy 1861 CACATATATCAANAGTGAGAAATGCCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 Db 1861 CACATATATCAANAGTGAGAAATGCCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 Qy 1921 TGACCTACTTTGGTAGTGGAAATAGTGAATTTACTATTAATTTGACTGAATATGTAGCT 1980
 Db 1921 TGACCTACTTTGGTAGTGGAAATAGTGAATTTACTATTAATTTGACTGAATATGTAGCT 1980
 Qy 1981 CATCCTTTACACCAACTCCTAAATTTTAAATAATTTCTACTCTCTCTTAATGAGAAAGTAC 2040
 Db 1981 CATCCTTTACACCAACTCCTAAATTTTAAATAATTTCTACTCTCTCTTAATGAGAAAGTAC 2040
 Qy 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGG 2100
 Db 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGG 2100
 Qy 2101 AGACCGAGTCTTGCTCTGTTACCCAGGCTGGAGTGGAGTGGTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTTGCTCTGTTACCCAGGCTGGAGTGGAGTGGTGGCTCACTGCA 2160
 Qy 2161 AGCTCTGCCCTCCCGGGTGGCAGCAATTCCTGCTCAGCTCAGCTCCCAATAGCTTGGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTGGCAGCAATTCCTGCTCAGCTCAGCTCCCAATAGCTTGGCC 2220
 Qy 2221 TACAGTCACTGCCACACACACTGGCTAAATTTTGTACTTTTAGTAGACAGGGTTTC 2280
 Db 2221 TACAGTCACTGCCACACACACTGGCTAAATTTTGTACTTTTAGTAGACAGGGTTTC 2280
 Qy 2281 ACCGTGTTAGCCAGAGTGGTCTCGATCTCTGACCTCGTATCCGCCACCTCGGCTCC 2340
 Db 2281 ACCGTGTTAGCCAGAGTGGTCTCGATCTCTGACCTCGTATCCGCCACCTCGGCTCC 2340
 Qy 2341 CAAGTGTCTGGGATTACAGGATGAGCCAGG 2372
 Db 2341 CAAGTGTCTGGGATTACAGGATGAGCCAGG 2372

RESULT 9
 AAV03607
 ID AAV03607 standard; cdna; 2372 bp.
 XX
 AC AAV03607;
 XX
 DT 29-APR-1998 (first entry)
 XX
 DE cdna sequence of human MDM2.
 XX
 KW MDM2; tumour; diagnosis; neoplasia; DNA binding protein;
 KW p53 polypeptide; binding; tumour cell; p53-regulated growth;
 KW inhibition; anti-cancer agent; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CD5 312..1787
 FT /*tag= a

XX US5702903-A.
 XX 30-DEC-1997.
 XX 13-NOV-1995; 9505-0557393.
 XX 07-APR-1993; 93US-0044619.
 XX 07-APR-1992; 92US-0867840.
 XX 23-JUN-1992; 92US-0903103.
 XX 18-MAY-1994; 94US-0245500.
 XX (UJYO) UNIV JOHNS HOPKINS.
 XX Kinzler KW, Vogelstein B;
 XX WPI; 1998-076411/07.
 XX P-PSDB; AAW42971.
 XX Cell containing reporter construct containing human MDM2 and p53
 XX genes - for identifying compounds that interfere with binding of
 XX human MDM2 to human p53, useful as anti-cancer agents
 XX Disclosure; Coulms 21-26; 37pp; English.
 XX The present sequence encodes human MDM2. The MDM2 gene is amplified in
 XX some human tumours. The amplification of this gene is diagnostic of
 XX neoplasia or its potential. It is speculated that the MDM2 protein is a
 XX potential DNA binding protein that functions in the modulation of
 XX expression of other genes and, when present in excess, interferes with
 XX normal constraints on cell growth. A cell containing three recombinant
 XX DNA constructs was produced. These constructs encode an MDM2 protein
 XX fused to a sequence-specific DNA binding domain, a p53 polypeptide fused
 XX to a transcriptional activation domain, and a reporter gene downstream
 XX from a DNA element which is recognised by the sequence-specific
 XX DNA-binding domain. The cell is used to identify a compound which
 XX interferes with the binding of MDM2 and p53. Since MDM2 is overexpressed
 XX in tumour cells and since binding of MDM2 to p53 appears to allow tumour
 XX cells to escape from p53-regulated growth, compounds that inhibit such
 XX binding would be useful as anti-cancer agents.
 XX Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 19; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCACCGCGCAGCTGGCTGCTTCTGGGGGCTGTGTGGCCCTGTGTGCGGAAGATGGA 60
 Db 1 GCACCGCGCAGCTGGCTGCTTCTGGGGGCTGTGTGGCCCTGTGTGCGGAAGATGGA 60
 Qy 61 GCAAGAGCCGAGCCGAGGGGGGCGCGACCCCTCTGACCGAGATCTCTGCTGCTTTTCG 120
 Db 61 GCAAGAGCCGAGCCGAGGGGGGCGCGACCCCTCTGACCGAGATCTCTGCTGCTTTTCG 120
 Qy 121 CAGCCAGGACCCCTCCCTCCCGGATAGTGGTACGAGCCGCGAGTCCCTGCGCCG 180
 Db 121 CAGCCAGGACCCCTCCCTCCCGGATAGTGGTACGAGCCGCGAGTCCCTGCGCCG 180
 Qy 181 GAGAGTGGAAATGATCCCGAGGCGCGAGGGGCTGTGTCCCGAGTAGTCAGTCCCGCGT 240
 Db 181 GAGAGTGGAAATGATCCCGAGGCGCGAGGGGCTGTGTCCCGAGTAGTCAGTCCCGCGT 240
 Qy 241 AAGGAACTGGGGAGTCTTGAGGAGCCCGGACTCCAGCGCGAACCCTCCCGATGGTGA 300
 Db 241 AAGGAACTGGGGAGTCTTGAGGAGCCCGGACTCCAGCGCGAACCCTCCCGATGGTGA 300
 Qy 301 GGACGAGCAATCTGCAATACCAATCTGTGTACCTACTGATGGTGTGTAACACCT 360
 Db 301 GGACGAGCAATCTGCAATACCAATCTGTGTACCTACTGATGGTGTGTAACACCT 360
 Qy 361 CACAGATTCAGCTCGGAACAAGAGACCTGGTGTAGACCAAGGCCATGCTTTTGAAGT 420
 Db 361 CACAGATTCAGCTCGGAACAAGAGACCTGGTGTAGACCAAGGCCATGCTTTTGAAGT 420

Db 361 CACAGATTCAGCTCGGAACAAGAGACCTGGTGTAGACCAAGGCCATGCTTTTGAAGT 420
 Qy 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATATCTATGAAAGAGTCTTTTATC 480
 Db 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATATCTATGAAAGAGTCTTTTATC 480
 Qy 481 TTGGCCAGTATATATGACTAAAGGATTATATGATGAGAACAACAACATATTTATATT 540
 Db 481 TTGGCCAGTATATATGACTAAAGGATTATATGATGAGAACAACAACATATTTATATT 540
 Qy 541 GTTCAATGATCTTCTTAGGAGATTGTTTGGCGTCCAAAGCTTCTGTGAAAGAGCACA 600
 Db 541 GTTCAATGATCTTCTTAGGAGATTGTTTGGCGTCCAAAGCTTCTGTGAAAGAGCACA 600
 Qy 601 GGAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
 Db 601 GGAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
 Qy 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTACCTTTGAAAGTGGAGTGATCAAAAGG 720
 Db 661 ACTCAGGTACATCTGTGAGTGAGAACAGGTGTACCTTTGAAAGTGGAGTGATCAAAAGG 720
 Qy 721 ACCTTGTACAGAGCTTCAGGAAGAACCTTCTATCTTACATTTGGTTTCTAGACCAT 780
 Db 721 ACCTTGTACAGAGCTTCAGGAAGAACCTTCTATCTTACATTTGGTTTCTAGACCAT 780
 Qy 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
 Db 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
 Qy 841 GTGAACGACAAAGAAACGCCACAAATCTGATGATTTTCCCTTTTCTTTGATGAAAGCC 900
 Db 841 GTGAACGACAAAGAAACGCCACAAATCTGATGATTTTCCCTTTTCTTTGATGAAAGCC 900
 Qy 901 TGGCTCTCTGTATAGGGAGATATCTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 Db 901 TGGCTCTCTGTATAGGGAGATATCTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 Qy 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAATTCAGTGGTTGG 1020
 Db 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAATTCAGTGGTTGG 1020
 Qy 1021 ATCAGGATTCAGTTTCAGATCAGTTAGTGTAGATTTGAAGTTGAATCTCCACATCAG 1080
 Db 1021 ATCAGGATTCAGTTTCAGATCAGTTAGTGTAGATTTGAAGTTGAATCTCCACATCAG 1080
 Qy 1081 AAGATATAGCCTTAGTGAAGAGGACAACTCTCAGATGAAGATGATGAGGTATATC 1140
 Db 1081 AAGATATAGCCTTAGTGAAGAGGACAACTCTCAGATGAAGATGATGAGGTATATC 1140
 Qy 1141 AAGTTACTGTGTATCAGCGAGGGAGATGATACAGATTCATTTGAAGAGATCCTGAAA 1200
 Db 1141 AAGTTACTGTGTATCAGCGAGGGAGATGATACAGATTCATTTGAAGAGATCCTGAAA 1200
 Qy 1201 TTTCTCTAGCTGACATTTGGAAATGCACCTTCATGCAATGAATGAATCCCTTCCAT 1260
 Db 1201 TTTCTCTAGCTGACATTTGGAAATGCACCTTCATGCAATGAATGAATCCCTTCCAT 1260
 Qy 1261 CACATTCGAAACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCCTGAAGATAAAGGAAAG 1320
 Db 1261 CACATTCGAAACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCCTGAAGATAAAGGAAAG 1320
 Qy 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAACTCAACACAGCTCAAGAGGGCT 1380
 Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAACTGGAAACTCAACACAGCTCAAGAGGGCT 1380
 Qy 1381 TTGATGTTCCCTGATTTGAAAAAACTATAGTGAATGATTTCCAGAGAGTCTGTTGAGG 1440
 Db 1381 TTGATGTTCCCTGATTTGAAAAAACTATAGTGAATGATTTCCAGAGAGTCTGTTGAGG 1440
 Qy 1441 AAAATGATGATAAATTCACAGCTTCACAAATCACAAGAAAGTGAAGACTATTTCTCAGC 1500
 Db 1441 AAAATGATGATAAATTCACAGCTTCACAAATCACAAGAAAGTGAAGACTATTTCTCAGC 1500

QY 1501 CATCAACTTCTAGTAGCATTATTTATAGCAGCCAAAGAGATGTGAAAGAGTTTGAAGGG 1560
 Db 1501 CATCAACTTCTAGTAGCATTATTTATAGCAGCCAAAGAGATGTGAAAGAGTTTGAAGGG 1560
 QY 1561 AAGAAACCCCAAGCAAGAGAGTGTGGATCTAGTTTGGCCCTTAATGCCATTGAC 1620
 Db 1561 AAGAAACCCCAAGCAAGAGAGTGTGGATCTAGTTTGGCCCTTAATGCCATTGAC 1620
 QY 1621 CTTGTGTGATTTCTCAAGCTCGACCTAAATATGGTTGCAATGTCTCATGGCAAAACAGGAC 1680
 Db 1621 CTTGTGTGATTTCTCAAGCTCGACCTAAATATGGTTGCAATGTCTCATGGCAAAACAGGAC 1680
 QY 1681 ATCTTATGGCCCTTTACATGTGCAAGAGCTAAAGAAAGAGTAAGGCCCTGCCAG 1740
 Db 1681 ATCTTATGGCCCTTTACATGTGCAAGAGCTAAAGAAAGAGTAAGGCCCTGCCAG 1740
 QY 1741 TATGTAGCAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
 Db 1741 TATGTAGCAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTTGACCTGTCTAT 1800
 QY 1801 AAGAGAAATATATTTCTTAACATATATACCTAGGAATTTAGCAACCTGAATTTAT 1860
 Db 1801 AAGAGAAATATATTTCTTAACATATATACCTAGGAATTTAGCAACCTGAATTTAT 1860
 QY 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
 Db 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTCACATAGATTTCTTCTTTAGTATAT 1920
 QY 1921 TGACCTACTTTGGTGTGGAATAGCAATACATTAATTAATTTGACTTGAATATGTAGCT 1980
 Db 1921 TGACCTACTTTGGTGTGGAATAGCAATACATTAATTAATTTGACTTGAATATGTAGCT 1980
 QY 1981 CATCTTTACACCACTCTTAATTTAAATAATTTCTACTGTCTTAAATGAGAAGTAC 2040
 Db 1981 CATCTTTACACCACTCTTAATTTAAATAATTTCTACTGTCTTAAATGAGAAGTAC 2040
 QY 2041 TTGGTTTTTTTTTTCTTAATATGATATGACATTTAAATGAACTTATTAATTTTATTTT 2100
 Db 2041 TTGGTTTTTTTTTTCTTAATATGATATGACATTTAAATGAACTTATTAATTTTATTTT 2100
 QY 2101 AGACCGAGTCTTCTGTGTACCGAGCTGGAGTGCAGTGGTGTATCTTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTTCTGTGTACCGAGCTGGAGTGCAGTGGTGTATCTTGGCTCACTGCA 2160
 QY 2161 AGCTCTGCCCTCCCGGGTTCGACCAATTTCTCCTGCTCAGCTCCCAATAGCTTGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTCGACCAATTTCTCCTGCTCAGCTCCCAATAGCTTGCC 2220
 QY 2221 TACAGTCACTGCGCACACACCTGGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
 Db 2221 TACAGTCACTGCGCACACACCTGGCTAATTTTGTACTTTTGTAGAGACAGGGTTTC 2280
 QY 2281 ACCGTGTAGCCAGAGTGTCTGATCTCCTGACCTGTGATCCGCCACCTCGGCCCTCC 2340
 Db 2281 ACCGTGTAGCCAGAGTGTCTGATCTCCTGACCTGTGATCCGCCACCTCGGCCCTCC 2340
 QY 2341 CAAGTCTGGGATACAGGCATGACCCACCG 2372
 Db 2341 CAAGTCTGGGATACAGGCATGACCCACCG 2372

RESULT 10

AAZ37471

ID AAZ37471 standard; cDNA; 2372 BP.

AC AAZ37471;

XX AAZ37471;

DT 07-JAN-2000 (first entry)

DE Human sarcoma p53-associated gene.

XX Human mdm2 gene; proliferation; tumour; phosphorothioate; p53;

KW cancer; antisense; modulation; oligonucleotide; expression;
 KW inhibition; hyperproliferation; blood cancer; brain cancer;
 KW breast cancer; lung cancer; soft tissue cancer; psoriasis; fibrosis;
 KW atherosclerosis; restenosis; ss.
 XX Homo sapiens.
 OS
 PN WO9949065-A1.
 XX
 PD 30-SEP-1999.
 XX
 PF 26-MAR-1999; 99WO-US06702.
 XX
 PR 26-MAR-1998; 98US-0048810.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowser LM;
 XX WPI; 1999-610754/52.
 XX
 PT New antisense compounds used to treat eg. hyperproliferative conditions
 XX
 PS Example 2; Page 79-81; 157pp; English.
 XX
 CC AAZ37473-237738 represent human mdm2 phosphorothioate oligonucleotides.
 CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
 CC exemplification of the present invention. The present invention
 CC describes novel nucleotide antisense compounds, targeted to the 5'
 CC untranslated, translation termination codon, or 3' untranslated region
 CC of a nucleic acid encoding human mdm2, that modulates expression of
 CC human mdm2. The oligonucleotides mediate their effect by antisense
 CC inhibition of hyperproliferative gene expression. The antisense compound
 CC is used to treat an animal having a disease or condition associated
 CC with mdm2, particularly a hyperproliferative condition, more
 CC particularly cancer, especially of the blood, brain, breast, lung or soft
 CC tissue, or psoriasis, fibrosis, atherosclerosis or restenosis.
 XX
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 20; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCACCCGCGAGCTTGGCTTCTTGGGCGCTGTGTGGCCCTGTGTGCGAAGATGGA 60
 Db 1 GCACCCGCGAGCTTGGCTTCTTGGGCGCTGTGTGGCCCTGTGTGCGAAGATGGA 60
 QY 61 GCAAGAGCCGAGCCCGAGGCGCGCCGACCCCTGACCGAGATCCTGCTGCTTCG 120
 Db 61 GCAAGAGCCGAGCCCGAGGCGCGCCGACCCCTGACCGAGATCCTGCTGCTTCG 120
 QY 121 CAGCCAGGAGCAGCTTCCCTCCCGGATTTAGTGTGCGTACGAGCGCCAGTCCGCTGGCCG 180
 Db 121 CAGCCAGGAGCAGCTTCCCTCCCGGATTTAGTGTGCGTACGAGCGCCAGTCCGCTGGCCG 180
 QY 181 GAGAGTGGATGATCCCGAGGCGCGCCGAGGCGCTGTGTGCGTACGAGTGTGCTGCTGCTG 240
 Db 181 GAGAGTGGATGATCCCGAGGCGCGCCGAGGCGCTGTGTGCGTACGAGTGTGCTGCTGCTG 240
 QY 241 AAGGAACTGGGAGTCTTTGAGGAGCCCGGACCTCCAGCGGAAACCCCGGATGTGA 300
 Db 241 AAGGAACTGGGAGTCTTTGAGGAGCCCGGACCTCCAGCGGAAACCCCGGATGTGA 300
 QY 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACCTACTGATGCTGTGAACCACT 360
 Db 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACCTACTGATGCTGTGAACCACT 360
 QY 361 CACAGATTCAGCTTCGGAAACAGAGACCTGTTAGACCAAGCCATTGCTTTGAAGT 420
 Db 361 CACAGATTCAGCTTCGGAAACAGAGACCTGTTAGACCAAGCCATTGCTTTGAAGT 420

QY 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATACATATGAAGAGGTTCTTTTTATC 480
 DB 421 TATTAAAGTCTGTTGGTGCACAAAAGACACTTATACATATGAAGAGGTTCTTTTTATC 480
 QY 481 TTGGCCAGTATATTAAGACTAAACGATATATGATGAGAAGCAACACATATTTATATT 540
 DB 481 TTGGCCAGTATATTAAGACTAAACGATATATGATGAGAAGCAACACATATTTATATT 540
 QY 541 GTTCAATGATCTTCTAGCAGATTTGTTGGGTGCCAAGCTTCTCTGTGAAGAGCACA 600
 DB 541 GTTCAATGATCTTCTAGCAGATTTGTTGGGTGCCAAGCTTCTCTGTGAAGAGCACA 600
 QY 601 GGAATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
 DB 601 GGAATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
 QY 661 ACTCAGGTACATCTGAGTGAGACAGGTCACCTTGAAGGTTGGGAGTGATCAAAAGG 720
 DB 661 ACTCAGGTACATCTGAGTGAGACAGGTCACCTTGAAGGTTGGGAGTGATCAAAAGG 720
 QY 721 ACCTTGTACAAGAGCTTCAAGGAGAGAACTTTCATCTTCACATTTGGTTTCTAGACCAT 780
 DB 721 ACCTTGTACAAGAGCTTCAAGGAGAGAACTTTCATCTTCACATTTGGTTTCTAGACCAT 780
 QY 781 CTACCTCATCTAGAAGGAGCAATAGTGAGACAGAGAAATTCAGATGAATATCTG 840
 DB 781 CTACCTCATCTAGAAGGAGCAATAGTGAGACAGAGAAATTCAGATGAATATCTG 840
 QY 841 GTGAACGACAAAAGCCACAACTCTGATAGTATTTCCCTTTCTTTCATGAAGGCC 900
 DB 841 GTGAACGACAAAAGCCACAACTCTGATAGTATTTCCCTTTCTTTCATGAAGGCC 900
 QY 901 TGGCTCTGTGTAAAGGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 DB 901 TGGCTCTGTGTAAAGGGAGATATGTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
 QY 961 GGAGCCCATCGAATCCGGATCTTGATGCTGTGTGAAGTGAACATTCAGGTCGATTTGG 1020
 DB 961 GGAGCCCATCGAATCCGGATCTTGATGCTGTGTGAAGTGAACATTCAGGTCGATTTGG 1020
 QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAAGTGAATCTCTGACTCAG 1080
 DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTGAATTTGAAGTGAATCTCTGACTCAG 1080
 QY 1081 AAGATTATACCTTGTAGTGAAGAGGACAACTCTCAGATCAAGATGATGAGGTATATC 1140
 DB 1081 AAGATTATACCTTGTAGTGAAGAGGACAACTCTCAGATCAAGATGATGAGGTATATC 1140
 QY 1141 AAGTTACTGTGTATCAGGCGAGGAGTGATACAGATTCATTTGAAGAAGATCCTGAAA 1200
 DB 1141 AAGTTACTGTGTATCAGGCGAGGAGTGATACAGATTCATTTGAAGAAGATCCTGAAA 1200
 QY 1201 TTTCCCTTAGCTGACTATTTGGAATGACATTCATGCAATGAATGAATCCCTTCCAT 1260
 DB 1201 TTTCCCTTAGCTGACTATTTGGAATGACATTCATGCAATGAATGAATCCCTTCCAT 1260
 QY 1261 CACATTCGAACAGATTTGGGCCCTTCTGTGAGAAATTTGGCTTCCCTGAAGATAAAGGGAAG 1320
 DB 1261 CACATTCGAACAGATTTGGGCCCTTCTGTGAGAAATTTGGCTTCCCTGAAGATAAAGGGAAG 1320
 QY 1321 ATAAGGGGAAATCTCTGAGAAGCCAACTGGAATTCACACAACTGGAAGGGCT 1380
 DB 1321 ATAAGGGGAAATCTCTGAGAAGCCAACTGGAATTCACACAACTGGAAGGGCT 1380
 QY 1381 TTGATGTTCTGATTTGAAAAAATATAGTGAATGATTTCCAGAGTCAATGTTGAGG 1440
 DB 1381 TTGATGTTCTGATTTGAAAAAATATAGTGAATGATTTCCAGAGTCAATGTTGAGG 1440
 QY 1441 AAAATGATGATAAATTTACAAAGCTTCAATATCAAGAAAGTGAAGACTATTTCTCAGC 1500
 DB 1441 AAAATGATGATAAATTTACAAAGCTTCAATATCAAGAAAGTGAAGACTATTTCTCAGC 1500
 QY 1501 CATCAACTTCTAGTACATTTATATAGCAGCCCAAGATGTGAAGAGTTTGAAGGG 1560

DB 1501 CATCAACTTCTAGTACATTTATATAGCAGCCCAAGAGATGTGAAGAGTTTGAAGGG 1560
 QY 1561 AAAAAACCAAGACAAAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
 DB 1561 AAAAAACCAAGACAAAAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
 QY 1621 CTTGTGTGATTTGTCAAGGTGCAGCTTAAATGTTGCATTTGCATTTGCAAAACAGGAC 1680
 DB 1621 CTTGTGTGATTTGTCAAGGTGCAGCTTAAATGTTGCATTTGCAAAACAGGAC 1680
 QY 1681 ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAAGAAAGAAATAGCCCTGCCAG 1740
 DB 1681 ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAAGAAAGAAATAGCCCTGCCAG 1740
 QY 1741 TATGTAGACAAACCAATTCAAATGATTGTCTAACTTATTTCCCTTACCTGCTGCTAT 1800
 DB 1741 TATGTAGACAAACCAATTCAAATGATTGTCTAACTTATTTCCCTTACCTGCTGCTAT 1800
 QY 1801 AAGAAATATATATTTCTAACTATATTAACCTTAGGAATTTAGACAACTGAAATTTATT 1860
 DB 1801 AAGAAATATATATTTCTAACTATATTAACCTTAGGAATTTAGACAACTGAAATTTATT 1860
 QY 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 DB 1861 CACATATATCAAGTGAGAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
 QY 1921 TGACCTTACTTTTGGTAGTGAATAGTAACTTACTTAAATTTGACTTGAATGTAGCT 1980
 DB 1921 TGACCTTACTTTTGGTAGTGAATAGTAACTTACTTAAATTTGACTTGAATGTAGCT 1980
 QY 1981 CATCTTTACCAACTCTTAAATTTAAATTAATTTCTACTCTGTCTTAAATGAGAGTAC 2040
 DB 1981 CATCTTTACCAACTCTTAAATTTAAATTAATTTCTACTCTGTCTTAAATGAGAGTAC 2040
 QY 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATTAATTTATTTTATTTTGG 2100
 DB 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATTAATTTATTTTATTTTGG 2100
 QY 2101 AGACCGAGTCTTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCAGTGA 2160
 DB 2101 AGACCGAGTCTTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCAGTGA 2160
 QY 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCTCAGCCTCCCAATTAGCTTGGCC 2220
 DB 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCTCAGCCTCCCAATTAGCTTGGCC 2220
 QY 2221 TACAGTCACTCTGCCACACACCTGGCTAAATTTTGTACTTTTAGTAGACAGAGGTTTC 2280
 DB 2221 TACAGTCACTCTGCCACACACCTGGCTAAATTTTGTACTTTTAGTAGACAGAGGTTTC 2280
 QY 2281 ACCGTCTTAGCCAGGATGCTCTGATCTCTGACCTGATCGCCACCTCGGCCCTCC 2340
 DB 2281 ACCGTCTTAGCCAGGATGCTCTGATCTCTGACCTGATCGCCACCTCGGCCCTCC 2340
 QY 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
 DB 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

RESULT 11

AX35093
 -ID AX35093 standard; cDNA; 2372 BP.

XX AX35093;

XX 01-JUL-1999 (first entry)

XX Nucleotide sequence of human MDM2 cDNA.

XX MDM2 protein; antisense oligonucleotide; activate; tumour suppressor;
 XX Inhibition; tumour growth; DNA-damaging agent; camptothecin; ss.

OS Homo sapiens.
XX W09910486-A2.
XX 04-MAR-1999.
XX 18-AUG-1998; 98WO-US17147.
XX 06-MAY-1998; 98US-0073567.
XX 22-AUG-1997; 97US-0916384.
XX (HYBR-) HYBRIDON INC.
XX Agrawal S, Chen J, Zhang R;
XX WPI; 1999-254219/21.
XX New MDM2-specific antisense oligonucleotides
XX Disclosure; Fig 1A; 59pp; English.
XX
XX The present sequence represents the cDNA sequence encoding human MDM2
XX protein. The specification describes antisense oligonucleotides that
XX inhibit MDM2 protein expression. The antisense oligonucleotides can
XX be used to activate a tumour suppressor. The antisense oligonucleotides
XX are used to inhibit tumour growth in a mammal, including a human,
XX particularly in conjunction with a DNA-damaging agent such as
XX camptothecin.
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 20; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGGCCCTGTGTGGAAAGATGGA 60
DB 1 GCACCGCGCAGCTTGGCTGCTTCTGTGGGCGCTGTGTGGCCCTGTGTGGGAAAGATGGA 60
QY 61 GCAAGAAAGCCGAGCCGAGGCGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
DB 61 GCAAGAAAGCCGAGCCGAGGCGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120
QY 121 CAGCCAGGACCGCTTCCCTCCCGATAGTGTGCTAGCGGCCCGCTGCTGCTGCGCCG 180
DB 121 CAGCCAGGACCGCTTCCCTCCCGATAGTGTGCTAGCGGCCCGCTGCTGCTGCGCCG 180
QY 181 GAGAGTGGAAATGATCCCGAGGCGCCAGGCGCTGCTTCCGCAATAGTCACTGCTCCCGTG 240
DB 181 GAGAGTGGAAATGATCCCGAGGCGCCAGGCGCTGCTTCCGCAATAGTCACTGCTCCCGTG 240
QY 241 AAGGAAACTGGGAGTCTTGGAGGACCCCGGACCTCCAAAGCGGAAACCCCGGATGGA 300
DB 241 AAGGAAACTGGGAGTCTTGGAGGACCCCGGACCTCCAAAGCGGAAACCCCGGATGGA 300
QY 301 GGACGAGCAATGTGCAATACCAATGCTGTACCTACTGTAGTGGTGTGCTGTACCACT 360
DB 301 GGACGAGCAATGTGCAATACCAATGCTGTACCTACTGTAGTGGTGTGCTGTACCACT 360
QY 361 CACAGATTCAGCTTCGGAAACAGAGACCCCTGGTGTAGCAAGCAATGCTTGTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAAACAGAGACCCCTGGTGTAGCAAGCAATGCTTGTGAAGT 420
QY 421 TATTAAAGTCTGTGGTGCACAAAGACACTTATACCTATGAAAGAGTCTTTTATC 480
DB 421 TATTAAAGTCTGTGGTGCACAAAGACACTTATACCTATGAAAGAGTCTTTTATC 480
QY 481 TTGCCAGTATATTGACTTAACGATTATATGATGAGAAGCAACATATTGTATTT 540
DB 481 TTGCCAGTATATTGACTTAACGATTATATGATGAGAAGCAACATATTGTATTT 540
QY 541 GTTCAATGATCTTAGGAGATTTGTTGGCGTCCAGCTTCTCTGTGAAGAGCACA 600
DB 541 GTTCAATGATCTTAGGAGATTTGTTGGCGTCCAGCTTCTCTGTGAAGAGCACA 600

DB 541 GTTCAATGATCTTAGGAGATTTGTTGGCGTCCAGCTTCTCTGTGAAGAGCACA 600
QY 601 GGAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
DB 601 GGAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
QY 661 ACTCAGGTACATCTGTGAGTGAAGACAGGTGTACCTTGAAGGTGGAGTGAAGG 720
DB 661 ACTCAGGTACATCTGTGAGTGAAGACAGGTGTACCTTGAAGGTGGAGTGAAGG 720
QY 721 ACCTTGTACAGAGCTTTCAGGAAGAGAACTTTCATCTTCACATTTGGTTCTAGACCAT 780
DB 721 ACCTTGTACAGAGCTTTCAGGAAGAGAACTTTCATCTTCACATTTGGTTCTAGACCAT 780
QY 781 CTACCTCATCTAGAGGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
DB 781 CTACCTCATCTAGAGGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
QY 841 GTGAACGACAAAGAAACCCCAAAATCTGATATTTTCCCTTTCTTTGATGAAGCC 900
DB 841 GTGAACGACAAAGAAACCCCAAAATCTGATATTTTCCCTTTCTTTGATGAAGCC 900
QY 901 TGGCTCTGTGTGTAATAGGAGATATTTGTGAAAGAGCAGTAGCAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTGTAATAGGAGATATTTGTGAAAGAGCAGTAGCAGTGAATCTACAG 960
QY 961 GGAGCCCATCGAATCCGGATCTTGATGCTGCTGTAAGTGAACATTTCAAGTGTGTTGG 1020
DB 961 GGAGCCCATCGAATCCGGATCTTGATGCTGCTGTAAGTGAACATTTCAAGTGTGTTGG 1020
QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAGAATTTGAAATCTCTCGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTGTAGTAGAATTTGAAATCTCTCGACTCAG 1080
QY 1081 AAGATTTATACCTTGTGTAAGAGCAAGAACTCTCAGATGAAGATGATGAGTATATC 1140
DB 1081 AAGATTTATACCTTGTGTAAGAGCAAGAACTCTCAGATGAAGATGATGAGTATATC 1140
QY 1141 AAGTTACTGTGTATCAGGCGGAGAGTGTATACAGATTTCAATTTGAAGAGATCTCTGAA 1200
DB 1141 AAGTTACTGTGTATCAGGCGGAGAGTGTATACAGATTTCAATTTGAAGAGATCTCTGAA 1200
QY 1201 TTTCTTTAGTGTACTTGTGAAATGCATCTTCATGCAATGAATGAATCCCTTCCAT 1260
DB 1201 TTTCTTTAGTGTACTTGTGAAATGCATCTTCATGCAATGAATGAATCCCTTCCAT 1260
QY 1261 CACATTCGAACAGATGTTGGGCCCTTCGTGAGAAATTTGCTTCTCTGAAAGTAAAGGAAAG 1320
DB 1261 CACATTCGAACAGATGTTGGGCCCTTCGTGAGAAATTTGCTTCTCTGAAAGTAAAGGAAAG 1320
QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCAAACTGGAAGAACTCAACACAGCTGAAGAGGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCAAACTGGAAGAACTCAACACAGCTGAAGAGGGCT 1380
QY 1381 TTGATGTTCTGATTTTAAAGAACTATAGTGAATGATTTCCAGAGATCATGTTGAGG 1440
DB 1381 TTGATGTTCTGATTTTAAAGAACTATAGTGAATGATTTCCAGAGATCATGTTGAGG 1440
QY 1441 AAAATGATGATAAAATTTACAAAGCTTTCACATCAACAAAGTGAAGACTTATCTCAGC 1500
DB 1441 AAAATGATGATAAAATTTACAAAGCTTTCACATCAACAAAGTGAAGACTTATCTCAGC 1500
QY 1501 CATCACTTCTAGTACATTTATAGCGCCAGAGATGTCGAAGCTTTGAAAGGG 1560
DB 1501 CATCACTTCTAGTACATTTATAGCGCCAGAGATGTCGAAGCTTTGAAAGGG 1560
QY 1561 AAGAAACCCCAAGCAAGAGAGTGTGAATCTAGTTTCCCTTAAATGCCATTTGAAC 1620
DB 1561 AAGAAACCCCAAGCAAGAGAGTGTGAATCTAGTTTCCCTTAAATGCCATTTGAAC 1620
QY 1621 CTTGCTGTGATTTCTCAGGTGCGACCTTAAAGTGGTTCATTTGTCCTCCGCAACAGGAC 1680
DB 1621 CTTGCTGTGATTTCTCAGGTGCGACCTTAAAGTGGTTCATTTGTCCTCCGCAACAGGAC 1680

QY 1681 ATCTTATGCGCTGCTTACATGTGCAAGAAAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
 DB 1681 ATCTTATGCGCTGCTTACATGTGCAAGAAAGCTAAAGAAAGAAATAGCCCTGCCAG 1740
 QY 1741 TATGTAGACAACAATCAAAATGATGTGCTAACTTATTTCCCGCTAGTGCCTGCTAT 1800
 DB 1741 TATGTAGACAACAATCAAAATGATGTGCTAACTTATTTCCCGCTAGTGCCTGCTAT 1800
 QY 1801 AACAGAAATATATATTTCTTAACATATATAACCTTAGGAATTTAGACAACCTGAAATTTAT 1860
 DB 1801 AACAGAAATATATATTTCTTAACATATATAACCTTAGGAATTTAGACAACCTGAAATTTAT 1860
 QY 1861 CACATATATCAAGTAGAGAAAATGCTCAATTCACATAGATTTCTTCTTTTATAGTAAAT 1920
 DB 1861 CACATATATCAAGTAGAGAAAATGCTCAATTCACATAGATTTCTTCTTTTATAGTAAAT 1920
 QY 1921 TGACCTACTTTGGTAGTGAATAGTAATCTTACTATAATTTGACATTGAATATAGTAGCT 1980
 DB 1921 TGACCTACTTTGGTAGTGAATAGTAATCTTACTATAATTTGACATTGAATATAGTAGCT 1980
 QY 1981 CATCTTTTACCAACCTCTTAATTTTAAATTAATTTCTACTGCTCTTAAATGAGAAGTAC 2040
 DB 1981 CATCTTTTACCAACCTCTTAATTTTAAATTAATTTCTACTGCTCTTAAATGAGAAGTAC 2040
 QY 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTAATTTATTTTATTTT 2100
 DB 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTAATTTATTTTATTTT 2100
 QY 2101 AGACGAGTCTGCTCTGTATCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCAGTCA 2160
 DB 2101 AGACGAGTCTGCTCTGTATCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCAGTCA 2160
 QY 2161 AGCTGCTGCCCTCCCGGGTTCGCACCATCTCTGCTCTGCTCAAGCTCCCAATTAGCTGGCC 2220
 DB 2161 AGCTGCTGCCCTCCCGGGTTCGCACCATCTCTGCTCTGCTCAAGCTCCCAATTAGCTGGCC 2220
 QY 2221 TACAGTCACTGCGCACCACTGCTAAATTTTGTACTTTTGTAGACAGAGGTTTC 2280
 DB 2221 TACAGTCACTGCGCACCACTGCTAAATTTTGTACTTTTGTAGACAGAGGTTTC 2280
 QY 2281 ACCGTGTTAGCCAGGATGCTCTGATCTCTGATCTCTGATCGTATCGGCCACCTCGGCCCTCC 2340
 DB 2281 ACCGTGTTAGCCAGGATGCTCTGATCTCTGATCTCTGATCGTATCGGCCACCTCGGCCCTCC 2340
 QY 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
 DB 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

RESULT 12
 ID AAX03947
 XX AAX03947 standard; cDNA; 2372 BP.
 AC AAX03947;
 XX 13-APR-1999 (first entry)
 DE Human MDM2 encoding cDNA.
 KW Human; MDM2; p53; tumorigenesis; growth regulation; diagnosis;
 KW malignant fibrous histiocytoma; MFH; liposarcoma; ds.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 312..1787
 FT /*tag= a
 PN US5858976-A.
 XX 12-JAN-1999.
 XX

PF 14-FEB-1997; 97US-0801718.
 XX 07-APR-1993; 93US-0044619.
 PR 07-APR-1992; 92US-0867840.
 PR 23-JUN-1992; 92US-0903103.
 PR 17-FEB-1995; 95US-0390515.
 PR 14-FEB-1997; 97US-0801718.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Burrell M, Hill DE, Kinzler KW, Vogelstein B;
 PI WPI; 1999-152105/13.
 DR P-PSDB; AAW94304.
 XX
 PT Inhibiting growth of tumour cells having MDM2 gene amplification -
 PT with MDM2-binding p53 fragment
 PS Example 1; Column 19-24; 41pp; English.
 XX
 CC The present invention describes: (1) a method for inhibiting the growth
 CC of tumour cells which contain a human MDM2 gene amplification,
 CC comprising administering to the cells a DNA molecule that expresses a
 CC polypeptide consisting of a portion of p53 i.e. amino acids 13-41 of the
 CC 64 amino acid sequence given in AAW94303, the polypeptide being capable
 CC of binding to human MDM2 (see AAW94304); (2) a method as in (1) where
 CC the polypeptide lacks the homo-oligomerisation domain of p53; and (3) a
 CC method as in (1) where the polypeptide lacks amino acids 138-393 of p53.
 CC The method is useful for treating the following tumour types which have
 CC a MDM2 gene amplification: M-7 malignant fibrous histiocytoma (MFH),
 CC M-20 MFH, L-9 liposarcoma, KL7 liposarcoma, KL28 liposarcoma, KL30
 CC liposarcoma, and OSA-CL MFH. The present sequence encodes human MDM2.
 XX
 :SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.0%; Score 2372; DB 20; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 DB 1 GCACCGCGCAGCTTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAAGATGGA 60
 QY 61 GCAAGAACCGCAGCGCGAGGGCGCGCCCTCTGACCGAGATCCTGCTGCTTCG 120
 DB 61 GCAAGAACCGCAGCGCGAGGGCGCGCCCTCTGACCGAGATCCTGCTGCTTCG 120
 QY 121 CAGCCAGGACGACGCTCCCTCCCGGATAGTGTGCTAGAGGCGCCAGTGCCTGGCCG 180
 DB 121 CAGCCAGGACGACGCTCCCTCCCGGATAGTGTGCTAGAGGCGCCAGTGCCTGGCCG 180
 QY 181 GAGAGTGAATGATCCCGAGGCGCGCTGCTTCCCGAGTGTGCTAGTCCCGCTG 240
 DB 181 GAGAGTGAATGATCCCGAGGCGCGCTGCTTCCCGAGTGTGCTAGTCCCGCTG 240
 QY 241 AAGGAACTGGGAGCTTGTGGGACCCCGGCTCCAGCGGAAACCCCGGATGTTGA 300
 DB 241 AAGGAACTGGGAGCTTGTGGGACCCCGGCTCCAGCGGAAACCCCGGATGTTGA 300
 QY 301 GGAGCAGGCAAAATGTGCAATACCAATGCTGTACTACTGATGCTGTGCTGTAAACCACT 360
 DB 301 GGAGCAGGCAAAATGTGCAATACCAATGCTGTACTACTGATGCTGTGCTGTAAACCACT 360
 QY 361 CACAGATTCAGCTTCGGAACAAGACACCTGGTAGACCAAGCCATGCTTTTGAAGT 420
 DB 361 CACAGATTCAGCTTCGGAACAAGACACCTGGTAGACCAAGCCATGCTTTTGAAGT 420
 QY 421 TATTAAGTCTGTGTGTCACAAAAGACACTTATATGATGAGAGGTTCTTTTATC 480
 DB 421 TATTAAGTCTGTGTGTCACAAAAGACACTTATATGATGAGAGGTTCTTTTATC 480
 QY 481 TTGCCAGTATATATGACTAAACGATTATATGATGAGAGCAACCAATATGTTATTT 540

Db 481 TTGCCAGTATATATGACTAAACGNTATATATGATGAGACCAACAATATTTGATATTT 540
Qy 541 GTTCAAAATGATCTTCTAGAGAGATTTGTTGGCGTGCACAGCTTCTCTGTGAAAGACACA 600
Db 541 GTTCAAAATGATCTTCTAGAGAGATTTGTTGGCGTGCACAGCTTCTCTGTGAAAGACACA 600
Qy 601 GGAATAATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
Db 601 GGAATAATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG 660
Qy 661 ACTCAGGTACATCTGTGAGTGAAGACAGGTGTACACCTTGAAGGTGGAGTGATCAAAAGG 720
Db 661 ACTCAGGTACATCTGTGAGTGAAGACAGGTGTACACCTTGAAGGTGGAGTGATCAAAAGG 720
Qy 721 ACCTTGTACAAAGAGCTTTCAGGAAGAGAAACCTTTCATCTTTCACATTTGGTTTCTAGACCAT 780
Db 721 ACCTTGTACAAAGAGCTTTCAGGAAGAGAAACCTTTCATCTTTCACATTTGGTTTCTAGACCAT 780
Qy 781 CTACCTCATCTAGAAGGAGCAANTTACTGAGACAGAGAAATTCAGATGAATTTATCTG 840
Db 781 CTACCTCATCTAGAAGGAGCAANTTACTGAGACAGAGAAATTCAGATGAATTTATCTG 840
Qy 841 GTGAACGACAAAGAAACCCACAAATCTGATAGTATTTCCCTTTCCCTTTGATCAAGGCC 900
Db 841 GTGAACGACAAAGAAACCCACAAATCTGATAGTATTTCCCTTTCCCTTTGATCAAGGCC 900
Qy 901 TGGCTCTCTGTGTAATAGGAGAGATATGTTGTAAGAGAGCAGTAGCAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTAATAGGAGAGATATGTTGTAAGAGAGCAGTAGCAGTGAATCTACAG 960
Qy 961 GGAGGCCATCGAATCCGGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGTTGGTGG 1020
Db 961 GGAGGCCATCGAATCCGGATCTTGATGCTGTGTAAGTGAACATTCAGGTGATGTTGGTGG 1020
Qy 1021 ATCAGGAATCAGTTTCAGATCAGTTTGTAGTGAATTTGAAGTTGAATCTCTCGACTCAG 1080
Db 1021 ATCAGGAATCAGTTTCAGATCAGTTTGTAGTGAATTTGAAGTTGAATCTCTCGACTCAG 1080
Qy 1081 AAGATTATAGCTTGTAGTGAAGAGACAAAGTCTCAGATGAAGATGATGAGGTATATC 1140
Db 1081 AAGATTATAGCTTGTAGTGAAGAGACAAAGTCTCAGATGAAGATGATGAGGTATATC 1140
Qy 1141 AAGTTACTGTGTATCAGGCGGGAGAGTGTACAGATTTCAATTTGAAGAGATCCCTGAA 1200
Db 1141 AAGTTACTGTGTATCAGGCGGGAGAGTGTACAGATTTCAATTTGAAGAGATCCCTGAA 1200
Qy 1201 TTTCTTGTAGTGAATTTGGAATGCATTCATGCAATGAATCAATCCCGCTTCCAT 1260
Db 1201 TTTCTTGTAGTGAATTTGGAATGCATTCATGCAATGAATCAATCCCGCTTCCAT 1260
Qy 1261 CACATTTGCAACAGATCTTGGGCCCTTTCGTGAGAATTTGGCTTCCCTCAAGATAAAGGGAAG 1320
Db 1261 CACATTTGCAACAGATCTTGGGCCCTTTCGTGAGAATTTGGCTTCCCTCAAGATAAAGGGAAG 1320
Qy 1321 ATAAAGGGGAAATCTCTGAGAAGCCAACTGGAAGAACTCAACAAAGCTGAAGAGGGCT 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAAGCCAACTGGAAGAACTCAACAAAGCTGAAGAGGGCT 1380
Qy 1381 TTGATGTTCTGATTTGTAAGAAACTATAGTGAATTTCCAGAGAGTCAATGTTGAGG 1440
Db 1381 TTGATGTTCTGATTTGTAAGAAACTATAGTGAATTTCCAGAGAGTCAATGTTGAGG 1440
Qy 1441 AAAATGATGATAAAATACAAAGCTTTCACATCAACAAGAAAGTGAAGACTATTTCTCAGC 1500
Db 1441 AAAATGATGATAAAATACAAAGCTTTCACATCAACAAGAAAGTGAAGACTATTTCTCAGC 1500
Qy 1501 CATCAACTTCTAGTACATTTATAGCAGCCAAAGAGATGTGAAGAGTTTGAAGGG 1560
Db 1501 CATCAACTTCTAGTACATTTATAGCAGCCAAAGAGATGTGAAGAGTTTGAAGGG 1560
Qy 1561 AAGAAACCCAAAGACAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTGAAC 1620
Db 1561 AAGAAACCCAAAGACAAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTGAAC 1620

Qy 1621 CTTGTGTGATTTGTCAAGTGCACCTAAAAATGGTTGCAATTTGCCATGGCAAAACAGGAC 1680
Db 1621 CTTGTGTGATTTGTCAAGTGCACCTAAAAATGGTTGCAATTTGCCATGGCAAAACAGGAC 1680
Qy 1681 ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAAGAAAAGGAATAAGCCCTGCCAG 1740
Db 1681 ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAAGAAAAGGAATAAGCCCTGCCAG 1740
Qy 1741 TATGTAGACAACCAATTCAAATGATTTGCTTAACCTATTTTCCCTAGTTCACCTGTCTAT 1800
Db 1741 TATGTAGACAACCAATTCAAATGATTTGCTTAACCTATTTTCCCTAGTTCACCTGTCTAT 1800
Qy 1801 AAGAGAATTATATTTCTTAACTATATAACCTTAGGAATTTAGACAACCTGAAATTTAT 1860
Db 1801 AAGAGAATTATATTTCTTAACTATATAACCTTAGGAATTTAGACAACCTGAAATTTAT 1860
Qy 1861 CACATATATCAAGTGAGAAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
Db 1861 CACATATATCAAGTGAGAAAATGCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
Qy 1921 TGACCTACTTTGGTAGTGAATAGTGAATCTTACTATAATTTGACTTGAATATGAGCT 1980
Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATCTTACTATAATTTGACTTGAATATGAGCT 1980
Qy 1981 CATCCTTTACACCACTCTTAATTTTAAATTAATTTCTCTCTCTTAAATGAGAAGTAC 2040
Db 1981 CATCCTTTACACCACTCTTAATTTTAAATTAATTTCTCTCTCTTAAATGAGAAGTAC 2040
Qy 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTG 2100
Db 2041 TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTG 2100
Qy 2101 AGACCCAGCTTGTCTGTGTACCCAGGCTGAGTGCAGTGGGTGATCTTGGCTCAGTGCA 2160
Db 2101 AGACCCAGCTTGTCTGTGTACCCAGGCTGAGTGCAGTGGGTGATCTTGGCTCAGTGCA 2160
Qy 2161 AGCTCTGCCCCCTCCCGGGTTCCGACCATTCTCTGCTCAGCTCCCAATTTAGCTTGGCC 2220
Db 2161 AGCTCTGCCCCCTCCCGGGTTCCGACCATTCTCTGCTCAGCTCCCAATTTAGCTTGGCC 2220
Qy 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGTAGAGACAGGGTTTC 2280
Db 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGTAGAGACAGGGTTTC 2280
Qy 2281 ACCGTGTAGCCAGGATGCTCTCGATCTCTCAGCTCCGCTGATCCGCCACCTCGGCTCC 2340
Db 2281 ACCGTGTAGCCAGGATGCTCTCGATCTCTCAGCTCCGCTGATCCGCCACCTCGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTTACAGGCATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTTACAGGCATGAGCCACCG 2372

RESULT 13

AAA29389

ID AAA29389 standard; cDNA; 2372 BP.

XX AAA29389;

XX AC

XX AC

DT 12-SEP-2000 (first entry)

XX MD2 oncoprotein coding sequence.

XX

XX

KW hST2; telomerase; catalytic subunit; reverse transcriptase; life-span;

KW retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;

KW proliferation; immortal; tumour therapy; macular degeneration; activator;

KW INK4; ss.

XX

OS Homo sapiens.

XX

XX Key

FH Location/Qualifiers

FT 312..1787

| | | | |
|----|------|--|------|
| Db | 1261 | CACATTGCACAGATTGTGGGCCCTTCGTGAGAAATTCGGCTTCTCGAAGATAAAGGGAAAG | 1320 |
| Qy | 1321 | ATAAAGGGAAATCTCTGAGAAGCCAAACTGGAAGAACTCAACACAAAGCTGAAGAGGGCT | 1380 |
| Db | 1321 | ATAAAGGGAAATCTCTGAGAAGCCAAACTGGAAGAACTCAACACAAAGCTGAAGAGGGCT | 1380 |
| Qy | 1381 | TTGATGTTCCCTGATTGTAAAAAAACTATAGTGAATGATTCAGAGAGACTCATGTGTGAGG | 1440 |
| Db | 1381 | TTGATGTTCCCTGATTGTAAAAAAACTATAGTGAATGATTCAGAGAGACTCATGTGTGAGG | 1440 |
| Qy | 1441 | AAATGATGATAAAATTCACAAAGCTTCACAAATCACAAAGAAAGTGAAGACTTATCTCAGC | 1500 |
| Db | 1441 | AAATGATGATAAAATTCACAAAGCTTCACAAATCRCAAAGAAAGTGAAGACTTATCTCAGC | 1500 |
| Qy | 1501 | CATCAACTTCCTAGTAGCATTTATTAAGCAGCCAAAGAGATGTGAAGAGTTTGAAGAGG | 1560 |
| Db | 1501 | CATCAACTTCCTAGTAGCATTTATTAAGCAGCCAAAGAGATGTGAAGAGTTTGAAGAGG | 1560 |
| Qy | 1561 | AAGAAACCCAAAGACAAGAAGAGAGTGTGAATCTAGTTTGGCCCTTAAATGCCATTGAAC | 1620 |
| Db | 1561 | AAGAAACCCAAAGACAAGAAGAGAGTGTGAATCTAGTTTGGCCCTTAAATGCCATTGAAC | 1620 |
| Qy | 1621 | CTTGTGTGATTGTTCAAGGTCGACCTTAAATATGTTGCCATTTGCCATGGCAAAACAGAC | 1680 |
| Db | 1621 | CTTGTGTGATTGTTCAAGGTCGACCTTAAATATGTTGCCATTTGCCATGGCAAAACAGAC | 1680 |
| Qy | 1681 | ATCTTATGGCCGCTTTACATGTGCAAAAGAGCTTAAAGAAAAGAAATAGCCCTGCCAG | 1740 |
| Db | 1681 | ATCTTATGGCCGCTTTACATGTGCAAAAGAGCTTAAAGAAAAGAAATAGCCCTGCCAG | 1740 |
| Qy | 1741 | TATGTAGACAACCAATTCAAATGATTGTGCTAACTTATTTCCCTCCTAGTTGACCTGTCTAT | 1800 |
| Db | 1741 | TATGTAGACAACCAATTCAAATGATTGTGCTAACTTATTTCCCTCCTAGTTGACCTGTCTAT | 1800 |
| Qy | 1801 | AAGACAATTATATATTTCTTAACCTATATAACCCCTAGGAATTTAGACAACCTGAATTTAT | 1860 |
| Db | 1801 | AAGAGAATTATATATTTCTTAACCTATATAACCCCTAGGAATTTAGACAACCTGAATTTAT | 1860 |
| Qy | 1861 | CACATATATCAAGTGAAGAAATGGCTCAATTCACATAGATTTCTTCTCTTTAGTATAAT | 1920 |
| Db | 1861 | CACATATATCAAGTGAAGAAATGGCTCAATTCACATAGATTTCTTCTCTTTAGTATAAT | 1920 |
| Qy | 1921 | TGACCTACTTTGGTAGTGAATAGTAACTACTATATTTGACTTGAATATGTAGCT | 1980 |
| Db | 1921 | TGACCTACTTTGGTAGTGAATAGTAACTACTATATTTGACTTGAATATGTAGCT | 1980 |
| Qy | 1981 | CATCTTTTACCAACCTCTTAATTTTAAATAATTTCTACTCTCTTTAAAGAGAGATAC | 2040 |
| Db | 1981 | CATCTTTTACCAACCTCTTAATTTTAAATAATTTCTACTCTCTTTAAAGAGAGATAC | 2040 |
| Qy | 2041 | TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTATTTATTTTTTG | 2100 |
| Db | 2041 | TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTATTTATTTTTTG | 2100 |
| Qy | 2101 | AGACCGAGTCTTGCTGTGTACCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA | 2160 |
| Db | 2101 | AGACCGAGTCTTGCTGTGTACCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA | 2160 |
| Qy | 2161 | AGCTCTGCCCTTCCCGGGTTTCGGACCATTCCTCGCCTCAGCCTCCCAATTAGCTTGGCC | 2220 |
| Db | 2161 | AGCTCTGCCCTTCCCGGGTTTCGGACCATTCCTCGCCTCAGCCTCCCAATTAGCTTGGCC | 2220 |
| Qy | 2221 | TACAGTCTATCTGCCACCACACCTTGGCTAATTTTTTGTACTTTTGTAGTAGACAGAGTTTC | 2280 |
| Db | 2221 | TACAGTCTATCTGCCACCACACCTTGGCTAATTTTTTGTACTTTTGTAGTAGACAGAGTTTC | 2280 |
| Qy | 2281 | ACCGTGTTAGCCAGGATGCTCGATCTCCCTGACTCGTGATCCGCCACCTCGCCCTCC | 2340 |
| Db | 2281 | ACCGTGTTAGCCAGGATGCTCGATCTCCCTGACTCGTGATCCGCCACCTCGCCCTCC | 2340 |
| Qy | 2341 | CAAAGTCTGGGATTTACAGGCATGAGCCACCG | 2372 |
| Db | 2341 | CAAAGTCTGGGATTTACAGGCATGAGCCACCG | 2372 |

QY 61 GCAAGAAGCCGAGCCGAGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTGG 120
DB 61 GCAAGAAGCCGAGCCGAGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTGG 120
QY 121 CAGCCAGGAGCACGTCCTCCCGGATAGTGGGTAGAGCGGCCGCTGCGCCG 180
DB 121 CAGCCAGGAGCACGTCCTCCCGGATAGTGGGTAGAGCGGCCGCTGCGCCG 180
QY 181 GAGAGTGGAAATGATCCCGAGGCCGAGGGCGTCTGCTGCTCCGAGTAGTCAGTCCCGG 240
DB 181 GAGAGTGGAAATGATCCCGAGGCCGAGGGCGTCTGCTGCTCCGAGTAGTCAGTCCCGG 240
QY 241 AAGGAATCGGGAGTCTTGGAGGACCCCGGACTCCGAGCGGAGAAACCCCGGATGGTGA 300
DB 241 AAGGAATCGGGAGTCTTGGAGGACCCCGGACTCCGAGCGGAGAAACCCCGGATGGTGA 300
QY 301 GGAGCAGGCAAAATGTCGAATACCAACATGCTGTACCTACTGATGGTGTGAACACCT 360
DB 301 GGAGCAGGCAAAATGTCGAATACCAACATGCTGTACCTACTGATGGTGTGAACACCT 360
QY 361 CACAGATCCAGTTCGGAGAACAGAGACCCCTGGTTAGACCAAGCCATTCCTTTGAAGT 420
DB 361 CACAGATCCAGTTCGGAGAACAGAGACCCCTGGTTAGACCAAGCCATTCCTTTGAAGT 420
QY 421 TATTAAGTCTGTGTGTCACAAAAGACACTTATCTACTGATGGTGTGAACACCT 480
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QY 781 CTACCTCATCTAGAGGAGCAATAGTGAGACAGAAATTCAGATGAATATCTG 840
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DB 1261 CACATTCGAACAGATGTTGGGCCCTTCGTGAGAATTTGGCTTCTTGAAGATAAAGGGAAG 1320
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DB 1321 ATAAAGGGAAATCTCTGAGAAAGCCAACTGGAACCTCAACAAGCTGAAGAGGCT 1380
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Db 2341 CAAAGTCTGGGATTACAGGCATGAGCCACCG 2372

RESULT 15

AD07530

ID AAD07530 standard; DNA; 2372 BP.

XX

AC AAD07530;

DT 10-AUG-2001 (first entry)

XX Human p-53 associated mdm2 gene.

DE Human; mdm2 inhibitor; gene therapy; cell proliferation; therapeutic;

KW tumour; prophylaxis; ds.

RW Homo sapiens.

OS

PN US6238921-B1.

XX

XX 29-MAY-2001.

XX

XX 26-MAR-1998; 98US-0048810.

PF

PR 26-MAR-1998; 98US-0048810.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Miraglia LJ, Nero P, Graham MJ, Monia BP;

XX

DR WPI; 2001-366477/38.

XX

PT New oligonucleotides 16506, 16507, 16518, 16520, 16521, 16522 and

PT 16524, which inhibits human mdm2 expression, useful for inhibiting,

PT diagnosing or treating abnormal proliferative conditions associated

PT with mdm2 -

XX

XX Example 2; Column 19-24; 19pp; English.

PS

CC The present invention relates to compositions and methods for modulating

CC the expression of human mdm2 gene, a naturally present cellular gene

CC implicated in abnormal cell proliferation and tumour formation. The

CC invention also provides antisense oligonucleotides which are targeted

CC to the mdm2 gene and are capable of inhibiting the expression of mdm2

CC gene. The oligonucleotides are useful in diagnostics, therapeutics,

CC prophylaxis and as research reagents. They are especially useful for

CC inhibiting, diagnosing and treating abnormal proliferative conditions

CC associated with mdm2. The method is useful for detecting and determining

CC the role of mdm2 expression in various cell functions and physiological

CC processes and conditions, and for diagnosing conditions associated with

CC mdm2 expression. The present sequence is p-53 associated mdm2 gene from

CC human.

XX

SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 other;

Query Match 100.08; Score 2372; DB 22; Length 2372;

Best Local Similarity 100.08; Pred. No. 0;

Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCACCCGCGAGCTTGGCTGCTTCCTGCGGCCCTGTGTGSCCCTGTGTCTCGGAAGATGGA 60

Qy 61 GCAGAGCCGAGCCCGAGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTCG 120

Db 61 GCAGAGCCGAGCCCGAGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG 120

Qy 121 CAGCCAGAGACACCGTCCCTCCCGGATTAGTGGTAGAGCGCCAGTGCCCTGCGCCG 180

Db 121 CAGCCAGAGACACCGTCCCTCCCGGATTAGTGGTAGAGCGCCAGTGCCCTGCGCCG 180

Qy 181 GAGAGTGAATGATCCCGAGGCCCGAGGGCTCGTGTTCGCGAGTAGTCAGTCCCGCTG 240

Db 181 GAGAGTGAATGATCCCGAGGCCCGAGGGCTCGTGTTCGCGAGTAGTCAGTCCCGCTG 240

Qy 241 AAGAAACTGGGAGTCTTGAGGGACCCCGACCTCCAAAGCGGAAACCCCGATGGTGA 300

Db 241 AAGAAACTGGGAGTCTTGAGGGACCCCGACCTCCAAAGCGGAAACCCCGATGGTGA 300

Qy 301 GGAGCAGGCAAAATGTGCAATACCAACATGTGTACCTACTGTGTTGTTGATGTTGAT 360

Db 301 GGAGCAGGCAAAATGTGCAATACCAACATGTGTACCTACTGTGTTGTTGATGTTGAT 360

Qy 361 CACAGATTCAGCTTCGGAACAAGAGCCCTGTTAGACCAAGCCCATGCTTTTGAAGT 420

Db 361 CACAGATTCAGCTTCGGAACAAGAGCCCTGTTAGACCAAGCCCATGCTTTTGAAGT 420

Qy 421 TATTAAGTCTGTGTGTCACAAAAGACACTTATCTATGAAAGAGTTCCTTTTATC 480

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Qy 481 TTGGCCAGTATATGACTAAGCATTTATGATGAGAGACACACATATTGTATATT 540

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Qy 541 GTTCAAATGATCTCTAGGAGATTTGTTGGCGTGCCAAAGCTTCTCTGTGAAAGAGACA 600

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Qy 601 GGAAATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAGCAGGAATCATCG 660

Db 601 GGAAATATATACCATGATCTACAGAACTTGGTAGTAGTCAATCAGCAGGAATCATCG 660

Qy 661 ACTCAGGTACATCTGTGAGTGAACAAGCTGTACCTTGAAGTGGGAGTGATCAAAAG 720

Db 661 ACTCAGGTACATCTGTGAGTGAACAAGCTGTACCTTGAAGTGGGAGTGATCAAAAG 720

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Db 781 CTACCTCATCTAGAGGAGAGCAATTAGTAGACAGAGAAATTCAGATGAATTTATCTG 840

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Db 841 GTGACGCAAAAGAAACCCCAAAATCTGATAGTATTTCCTTCTTGTGATGAAAGCC 900

Qy 901 TGCGCTGTGTGTAAGGGAGATGTTGTGAAGACGAGTAGCAGTGAATCTACAG 960

Db 901 TGCGCTGTGTGTAAGGGAGATGTTGTGAAGACGAGTAGCAGTGAATCTACAG 960

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Qy 1021 ATCAGATTCAGTTTCAGATCAGTTTACTGTAGATTTGAGTTGAAATCTCGACTCAG 1080

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Qy 1081 AAGATTATACCTTGTGTAAGGACCAAGAACTCTCAGATGAAGATGATGAGTATATC 1140

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Qy 1141 AAGTTACTGTGATACAGGAGAGTGATACAGATTTTCAATTTGAAGAGATCCTGAA 1200

Db 1141 AAGTTACTGTGATACAGGAGAGTGATACAGATTTTCAATTTGAAGAGATCCTGAA 1200

[illegible]

Search completed: January 9, 2003, 11:00:40
Job time : 494 secs

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2003, 10:52:24 : Search time 87 Seconds
(without alignments)
8361.348 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcaacgcgcgcgttgctg.....attacaggcatgagccacg 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2.6/ptodata/2/ina/PC10S_COMB.seq.*
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 2372 | 100.0 | 2372 | 1 US-07-903-103-1 | Sequence 1, Appli |
| 2 | 2372 | 100.0 | 2372 | 1 US-08-044-619A-1 | Sequence 1, Appli |
| 3 | 2372 | 100.0 | 2372 | 1 US-08-283-911-1 | Sequence 1, Appli |
| 4 | 2372 | 100.0 | 2372 | 1 US-08-245-500A-2 | Sequence 2, Appli |
| 5 | 2372 | 100.0 | 2372 | 1 US-08-390-546-2 | Sequence 2, Appli |
| 6 | 2372 | 100.0 | 2372 | 1 US-08-390-479A-2 | Sequence 2, Appli |
| 7 | 2372 | 100.0 | 2372 | 1 US-08-557-393-2 | Sequence 2, Appli |
| 8 | 2372 | 100.0 | 2372 | 1 US-08-390-516C-2 | Sequence 2, Appli |
| 9 | 2372 | 100.0 | 2372 | 1 US-08-390-517A-2 | Sequence 2, Appli |
| 10 | 2372 | 100.0 | 2372 | 1 US-08-390-515A-2 | Sequence 2, Appli |
| 11 | 2372 | 100.0 | 2372 | 2 US-08-801-718-2 | Sequence 1, Appli |
| 12 | 2372 | 100.0 | 2372 | 3 US-09-073-567-1 | Sequence 1, Appli |
| 13 | 2372 | 100.0 | 2372 | 4 US-09-280-805-1 | Sequence 1, Appli |
| 14 | 2372 | 100.0 | 2372 | 4 US-09-048-810-1 | Sequence 1, Appli |
| 15 | 2372 | 100.0 | 2372 | 4 US-09-170-159A-2 | Sequence 2, Appli |
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| 19 | 975.6 | 41.1 | 1710 | 1 US-08-283-911-3 | Sequence 3, Appli |
| 20 | 975.6 | 41.1 | 1710 | 1 US-08-245-500A-4 | Sequence 4, Appli |
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| 22 | 975.6 | 41.1 | 1710 | 1 US-08-390-479A-4 | Sequence 4, Appli |
| 23 | 975.6 | 41.1 | 1710 | 1 US-08-557-393-4 | Sequence 4, Appli |
| 24 | 975.6 | 41.1 | 1710 | 1 US-08-390-516C-4 | Sequence 4, Appli |
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| 28 | 975.6 | 41.1 | 1710 | 3 US-09-073-567-12 | Sequence 12, Appli |
| 29 | 975.6 | 41.1 | 1710 | 4 US-09-170-159A-4 | Sequence 4, Appli |
| 30 | 975.6 | 41.1 | 1710 | 4 US-09-480-718-45 | Sequence 45, Appli |
| 31 | 812.4 | 34.2 | 891 | 4 US-09-167-322-5 | Sequence 5, Appli |
| 32 | 812.2 | 34.2 | 966 | 4 US-09-167-322-7 | Sequence 7, Appli |
| 33 | 652 | 27.5 | 652 | 4 US-09-510-252-3 | Sequence 3, Appli |
| 34 | 576 | 24.3 | 657 | 4 US-09-167-322-6 | Sequence 6, Appli |
| 35 | 313 | 13.2 | 399 | 4 US-09-167-322-8 | Sequence 8, Appli |
| 36 | 227.2 | 9.6 | 309 | 4 US-09-167-322-9 | Sequence 9, Appli |
| 37 | 223 | 9.4 | 3609 | 4 US-09-705-399-11 | Sequence 11, Appli |
| 38 | 219.6 | 9.3 | 246240 | 2 US-08-724-394A-20 | Sequence 20, Appli |
| 39 | 219.6 | 9.3 | 246240 | 2 US-08-724-394A-21 | Sequence 21, Appli |
| 40 | 219.6 | 9.3 | 246240 | 1 US-08-724-394A-22 | Sequence 22, Appli |
| 41 | 218.8 | 9.2 | 3742 | 1 US-08-694-915-5 | Sequence 5, Appli |
| 42 | 217.2 | 9.2 | 320 | 1 US-08-629-939-5 | Sequence 5, Appli |
| 43 | 217.2 | 9.2 | 320 | 1 US-08-759-873-5 | Sequence 5, Appli |
| 44 | 217.2 | 9.2 | 38564 | 4 US-09-734-673-3 | Sequence 3, Appli |
| 45 | 216 | 9.1 | 87543 | 4 US-09-791-211-3 | Sequence 3, Appli |

ALIGNMENTS

RESULT 1
US-07-903-103-1
; Sequence 1, Application US/07903103
; Patent No. 5411860
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDW2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920623
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/867.840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: CaCo-2
; POSITION IN GENOME:

; MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
US-07-903-103-1

Query March 100.0%; Score 2372; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1261 CACATTGCAACAGATGTGGGCCCTCTCGATGATGGCTTCTGAGATTAAGGAGAAAG 1320
Db 1261 CACATTGCAACAGATGTGGGCCCTCTCGATGATGGCTTCTGAGATTAAGGAGAAAG 1320

Qy 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTTGAAGAACTCAACACAGCTGAAGAGGCT 1380
Db 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTTGAAGAACTCAACACAGCTGAAGAGGCT 1380

Qy 1381 TTGATGTTCTTGATGTATTAAGAACTATAGTGAATGCCAGAGACTCATGTGTTGAGG 1440
Db 1381 TTGATGTTCTTGATGTATTAAGAACTATAGTGAATGCCAGAGACTCATGTGTTGAGG 1440

Qy 1441 AAAATGATGATAAAATACACAAGCTTCAACAATCAACAAGAAAGTGAAGACTTCTCAGC 1500
Db 1441 AAAATGATGATAAAATACACAAGCTTCAACAATCAACAAGAAAGTGAAGACTTCTCAGC 1500

Qy 1501 CATCAACTCTTAGTAGCATTTATAGCAGCCAGAGAGATGTGAAGAGTTTGAAGGG 1560
Db 1501 CATCAACTCTTAGTAGCATTTATAGCAGCCAGAGAGATGTGAAGAGTTTGAAGGG 1560

Qy 1561 AAGAAACCAAGACAAAGAGAGAGTGTGAATCTAGTTTGGCCCTTAAATGCCATTGAAC 1620
Db 1561 AAGAAACCAAGACAAAGAGAGAGTGTGAATCTAGTTTGGCCCTTAAATGCCATTGAAC 1620

Qy 1621 CTTGTGCTATTGTCAAGGTCGACCTAAATGGTGGCATTTGCCATGTCACAAACAGNC 1680
Db 1621 CTTGTGCTATTGTCAAGGTCGACCTAAATGGTGGCATTTGCCATGTCACAAACAGNC 1680

Qy 1681 ATCTTATGGCCTGCTTTACATGTGCAAAAGAGCTAAAGAAAGAAATAAGCCCTGCCAG 1740
Db 1681 ATCTTATGGCCTGCTTTACATGTGCAAAAGAGCTAAAGAAAGAAATAAGCCCTGCCAG 1740

Qy 1741 TATGTAGACAAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTTGACCTGCTAT 1800
Db 1741 TATGTAGACAAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTTGACCTGCTAT 1800

Qy 1801 AAGAGAAATATATATTTCTAACTATTAACCCCTAGGAATTTAGACAACTGAAATTAAT 1860
Db 1801 AAGAGAAATATATATTTCTAACTATTAACCCCTAGGAATTTAGACAACTGAAATTAAT 1860

Qy 1861 CACATATATCAAGTGAGAAATGCCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
Db 1861 CACATATATCAAGTGAGAAATGCCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920

Qy 1921 TGACCTACTTTGGTAGTGGAAATAGTAACTTACTATATAATTTGACTTCAATATGTAGCT 1980
Db 1921 TGACCTACTTTGGTAGTGGAAATAGTAACTTACTATATAATTTGACTTCAATATGTAGCT 1980

Qy 1981 CATCTCTTACACCAACTCCTTAATTTTAAATTAATTTCTACTCTCTTAAATGAGAGTAC 2040
Db 1981 CATCTCTTACACCAACTCCTTAATTTTAAATTAATTTCTACTCTCTTAAATGAGAGTAC 2040

| | | | |
|----|------|---|------|
| Qy | 2041 | TTGGTTTTTTTTTCTTAATAATGATATGACATTTAAAGTAACTATATATTTTTTGTG | 2100 |
| Db | 2041 | TTGGTTTTTTTTTCTTAATAATGATATGACATTTAAAGTAACTATATATTTTTTGTG | 2100 |
| Qy | 2101 | AGACCGAGCTCTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACGTGCA | 2160 |
| Db | 2101 | AGACCGAGCTCTGTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACGTGCA | 2160 |
| Qy | 2161 | AGCTCTGCCCTCCCGGGTTTCGACACATTCCTCCTGAGCTCAGCCTGCCAAATTTAGCTGGCC | 2220 |
| Db | 2161 | AGCTCTGCCCTCCCGGGTTTCGACACATTCCTCCTGAGCTCAGCCTGCCAAATTTAGCTGGCC | 2220 |
| Qy | 2221 | TACAGTCATCTGCCACACACACCTGGCTAAATTTTTTGTACTTTTTAGTAGAGACAGGGTTTC | 2280 |
| Db | 2221 | TACAGTCATCTGCCACACACACCTGGCTAAATTTTTTGTACTTTTTAGTAGAGACAGGGTTTC | 2280 |
| Qy | 2281 | ACCGTGTGTAGCCAGGATGGTCTCGATCTCCTGAGCTCGTGATCCGCCACCTCGGCCTCC | 2340 |
| Db | 2281 | ACCGTGTGTAGCCAGGATGGTCTCGATCTCCTGAGCTCGTGATCCGCCACCTCGGCCTCC | 2340 |
| Qy | 2341 | CAAAAGTCTGGGGATTACAGGCATGAGCCACCG | 2372 |
| Db | 2341 | CAAAAGTCTGGGGATTACAGGCATGAGCCACCG | 2372 |

RESULT 2

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US-08-044-619A-1
; Sequence 1, Application US/08044619A
; Patent No. 5420263
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; APPLICANT: 720 RUTLAND AVENUE, BALTIMORE, MARYLAND 21205 USA
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G ST., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/044,619A
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/903,103
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/867,840
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.40148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BMBB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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| | | | |
|----|------|--|------|
| Qy | 901 | TGGCTCTGTGTGTAATAAGGGAGATATGTTGTGAAAGACGACTAGCAGTGAATCTACAG | 960 |
| | | | |
| Db | 901 | TGGCTCTGTGTGTAATAAGGGAGATCTTGTGAAAGACGACTAGCAGTGAATCTACAG | 960 |
| | | | |
| Qy | 961 | GGACGCCATCGAATCCGGATCTTGATGCTGTGTAACTGAACATTCAGGTGATTTGGTTGG | 1020 |
| Db | 961 | GGACGCCATCGAATCCGGATCTTGATGCTGTGTAACTGAACATTCAGGTGATTTGGTTGG | 1020 |
| | | | |
| Qy | 1021 | ATCAGGATTCAGTTTCAGATCAGTTTGTGTAGAAATTTGAAGTTGAATCTCTCCACTCAG | 1080 |
| Db | 1021 | ATCAGGATTCAGTTTCAGATCAGTTTGTGTAGAAATTTGAAGTTGAATCTCTCCACTCAG | 1080 |
| | | | |
| Qy | 1081 | AAGATTATAGCCTTAGTGAAGAGGACAAAGAACTCTCAGATGAAGATGATGAGGTATATC | 1140 |
| Db | 1081 | AAGATTATAGCCTTAGTGAAGAGGACAAAGAACTCTCAGATGAAGATGATGAGGTATATC | 1140 |
| | | | |
| Qy | 1141 | AAGTTTACTGTGTATCAGGCAGGGGAGGTGATCAGATTTCATTTGAAGAGATCTGANA | 1200 |
| Db | 1141 | AAGTTTACTGTGTATCAGGCAGGGGAGGTGATCAGATTTCATTTGAAGAGATCTGANA | 1200 |
| | | | |
| Qy | 1201 | TTTCCTTAGCTGACTATTTGGAATGCACCTTCATCGAATGAATGAATCCCCCTTCCAT | 1260 |
| Db | 1201 | TTTCCTTAGCTGACTATTTGGAATGCACCTTCATCGAATGAATGAATCCCCCTTCCAT | 1260 |
| | | | |
| Qy | 1261 | CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCCTGAAGATAAAGGAAAG | 1320 |
| Db | 1261 | CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATGGCTTCCCTGAAGATAAAGGAAAG | 1320 |
| | | | |
| Qy | 1321 | ATAAAGGGGAAATCTCTGAGAAAGCCAACTCGAATGAATGAATCCCCCTTCCAT | 1380 |
| Db | 1321 | ATAAAGGGGAAATCTCTGAGAAAGCCAACTCGAATGAATGAATGAATCCCCCTTCCAT | 1380 |
| | | | |
| Qy | 1381 | TTGATGTTCCGTGATTTGTAATAAACTATAGTGAATGCCAGAGAGTCATGTGTTGAGG | 1440 |
| Db | 1381 | TTGATGTTCCGTGATTTGTAATAAACTATAGTGAATGCCAGAGAGTCATGTGTTGAGG | 1440 |
| | | | |
| Qy | 1441 | AAATGATGATAAATTTACACAAGCTTCACAATCACAAAGAAAGTGAAGACTATTCTCAGC | 1500 |
| Db | 1441 | AAATGATGATAAATTTACACAAGCTTCACAATCACAAAGAAAGTGAAGACTATTCTCAGC | 1500 |
| | | | |
| Qy | 1501 | CATCAACTTCTAGTAGCATTTATATAGCAGCCAAAGAGATGTGAAAGAGTTTGAAGAGG | 1560 |
| Db | 1501 | CATCAACTTCTAGTAGCATTTATATAGCAGCCAAAGAGATGTGAAAGAGTTTGAAGAGG | 1560 |
| | | | |
| Qy | 1561 | AAGAACCCAGACAAAGAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTGAC | 1620 |
| Db | 1561 | AAGAACCCAGACAAAGAGAGAGTGTGAATCTAGTTTGGCCCTTAATGCCATTGAC | 1620 |
| | | | |
| Qy | 1621 | CTTGTGTGATTTGTCAAGTGCACCTTAAAATGGTTGCATTTGCTCCATGCCAAACAGAC | 1680 |
| Db | 1621 | CTTGTGTGATTTGTCAAGTGCACCTTAAAATGGTTGCATTTGCTCCATGCCAAACAGAC | 1680 |
| | | | |
| Qy | 1681 | ATCTTATGCCCTGCTTTACATGTGCAAAGAAAGCTTAAAGAAAGGAATAGCCCTGCCAG | 1740 |
| Db | 1681 | ATCTTATGCCCTGCTTTACATGTGCAAAGAAAGCTTAAAGAAAGGAATAGCCCTGCCAG | 1740 |
| | | | |
| Qy | 1741 | TATGTAGACAACCAATTTCAATGATTTGCTTAACCTATTTCCTTGTGACCTGTCTAT | 1800 |
| Db | 1741 | TATGTAGACAACCAATTTCAATGATTTGCTTAACCTATTTCCTTGTGACCTGTCTAT | 1800 |
| | | | |
| Qy | 1801 | AAGAGAAATATATATTTCTTAACCTATATACCTCAGGAATTTAGACAACCTGAATTTAT | 1860 |
| Db | 1801 | AAGAGAAATATATATTTCTTAACCTATATACCTCAGGAATTTAGACAACCTGAATTTAT | 1860 |
| | | | |
| Qy | 1861 | CACATATATCAAGTGAAGAAATGCCCTCAATTCACATAGATTTCTTCTTTAGTATAT | 1920 |
| Db | 1861 | CACATATATCAAGTGAAGAAATGCCCTCAATTCACATAGATTTCTTCTTTAGTATAT | 1920 |
| | | | |
| Qy | 1921 | TGACCTACTTTGGTAGTGAATAGTACTTACTATAATTTGACTTGAATATGTAGCT | 1980 |
| Db | 1921 | TGACCTACTTTGGTAGTGAATAGTACTTACTATAATTTGACTTGAATATGTAGCT | 1980 |

| | | | |
|----|------|--|------|
| Qy | 1981 | CATCCTTTACACCAACTCCTTAATTTTTAAATAATTTCCTACTCTGCTCTAATAATGAGAAGTAC | 2040 |
| Db | 1981 | CATCCTTTACACCAACTCCCTAAATTTTAAATAATTTCCTACTCTGCTCTAATAATGAGAAGTAC | 2040 |
| Qy | 2041 | TTGGGTTTTTTTTTCTTTAAAATGTATATGACATTTAAATGTAACTTATTTATTTTTTTTG | 2100 |
| Db | 2041 | TTGGGTTTTTTTTTCTTTAAAATGTATATGACATTTAAATGTAACTTATTTATTTTTTTTG | 2100 |
| Qy | 2101 | AGACCGAGCTTGCCTCTGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCCA | 2160 |
| Db | 2101 | AGACCGAGCTTGCCTCTGTTTACCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCCA | 2160 |
| Qy | 2161 | AGCTCTGCCCTTCCC GG GTTGCACCAANTCTCTGCTCTAGCCTTCCCAATTTAGCTTGTGCC | 2220 |
| Db | 2161 | AGCTCTGCCCTTCCC GG GTTGCACCAANTCTCTGCTCTAGCCTTCCCAATTTAGCTTGTGCC | 2220 |
| Qy | 2221 | TACAGTGCATCTGCCACCAACACCACTTGGCTAAATTTTTTGTACTTTTTAGTAGAGACAGAGGTTTC | 2280 |
| Db | 2221 | TACAGTGCATCTGCCACCAACACCACTTGGCTAAATTTTTTGTACTTTTTAGTAGAGACAGAGGTTTC | 2280 |
| Qy | 2281 | ACGGTGTTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGNATCGGCCACCTCTCGGCCTCC | 2340 |
| Db | 2281 | ACGGTGTTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGNATCGGCCACCTCTCGGCCTCC | 2340 |
| Qy | 2341 | CAAAGTCTGGGGATTACAGGCATGAGCCACCG | 2372 |
| Db | 2341 | CAAAGTCTGGGGATTACAGGCATGAGCCACCG | 2372 |

RESULT 3

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US-08-283-911-1
: Sequence 1, Application US/08283911
: Patent No. 5519118
: GENERAL INFORMATION:
: APPLICANT: VOGELSTEIN, BERT
: APPLICANT: KINZLER, KENNETH
: TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
: TITLE OF INVENTION: HUMAN TUMORS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
: STREET: 1001 G ST., N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20001-4597
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/283,911
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/903,103
: FILING DATE: 23-JUN-1992
: APPLICATION NUMBER: US 07/867,840
: FILING DATE: 07-APR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: KAGAN, SARAH A.
: REGISTRATION NUMBER: 32,141
: REFERENCE/DOCKET NUMBER: 01107.40148
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-508-9100
: TELEFAX: 202-508-9299
: TELEX: 197430 BBMB UT
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2372 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: CaCo-2
; POSITION IN GENOME:
; MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
; US-08-283-911-1

Query Match      100.0%; Score 2372; DB 1: Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGAGCTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGGAAGATGCA 60
DB 1 GCACCGCGAGCTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGGAAGATGCA 60

QY 61 GCAAGAACGCGAGCGCGGCGCGCGACCCCTCTGACCGAGATCTCTGCTGCTTCG 120
DB 61 GCAAGAACGCGAGCGCGGCGCGCGACCCCTCTGACCGAGATCTCTGCTGCTTCG 120

QY 121 CACCGAGGAGCAGCTCCCTCCCGGATTTAGTGGTACGAGCGCCAGTCCCTGGCCG 180
DB 121 CACCGAGGAGCAGCTCCCTCCCGGATTTAGTGGTACGAGCGCCAGTCCCTGGCCG 180

QY 181 GAGAGTGGAAATGATCCCGAGCGCCGAGCGCTGTCTCCGCACTAGTCACTCCCGTG 240
DB 181 GAGAGTGGAAATGATCCCGAGCGCCGAGCGCTGTCTCCGCACTAGTCACTCCCGTG 240

QY 241 AAGGAACTGGGAGTCTTTGGGAGACCCCGACTCCAAAGCGGAAACCCCGATGGTA 300
DB 241 AAGGAACTGGGAGTCTTTGGGAGACCCCGACTCCAAAGCGGAAACCCCGATGGTA 300

QY 301 GGAGCGGCAATGTGCAATACCAATGCTGTGTACCTACTGTATGATGGTGTAAACACCT 360
DB 301 GGAGCGGCAATGTGCAATACCAATGCTGTGTACCTACTGTATGATGGTGTAAACACCT 360

QY 361 CACAGATTCAGCTTCGGAACAGAGACCTGGTTAGACAAAGCCATTCCTTTTCAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAGAGACCTGGTTAGACAAAGCCATTCCTTTTCAAGT 420

QY 421 TATTAAGTCTGTGGTCACAAAAGACACTTATCTATGAAGAGGTTCTTTTATTC 480
DB 421 TATTAAGTCTGTGGTCACAAAAGACACTTATCTATGAAGAGGTTCTTTTATTC 480

QY 481 TTGGCCAGTATATTGACTAACAGATTATATGATGAGAGCAACACATATTGTATTT 540
DB 481 TTGGCCAGTATATTGACTAACAGATTATATGATGAGAGCAACACATATTGTATTT 540

QY 541 GTTCAATGATCTCTAGGAGATTGTTGGCTGCCAGCTCTCTGTCAAGAGCACA 600
DB 541 GTTCAATGATCTCTAGGAGATTGTTGGCTGCCAGCTCTCTGTCAAGAGCACA 600

QY 601 GGAATATATACCATGATCTACAGAACTTTGGTAGTAGTCAATACAGAGAAATCATCG 660
DB 601 GGAATATATACCATGATCTACAGAACTTTGGTAGTAGTCAATACAGAGAAATCATCG 660

QY 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGTACCTTTGAAGTGGGAGTGAAGAGG 720
DB 661 ACTCAGTACATCTGTGAGTGAAGACAGGTGTACCTTTGAAGTGGGAGTGAAGAGG 720

QY 721 ACCTTGTACAGAGCTTACAGAGAGAAACCTTCACTTTCACATTTGGTTTTCAGACCAT 780
DB 721 ACCTTGTACAGAGCTTACAGAGAGAAACCTTCACTTTCACATTTGGTTTTCAGACCAT 780

QY 781 CTACCTCATCTAGAGGAGCAATTTAGTGAAGAGAGAAATTTAGATGAATTTCTG 840
DB 781 CTACCTCATCTAGAGGAGCAATTTAGTGAAGAGAGAAATTTAGATGAATTTCTG 840

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QY 841 GTGACGCAAGAAAGAAACGCCACAAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC 900
DB 841 GTGACGCAAGAAAGAAAGCCACAAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC 900

QY 901 TGGCTCTGTGTCTAATAAGGGAGATATCTCTGAAAGAACGACGTAGCAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTCTAATAAGGGAGATATCTCTGAAAGAACGACGTAGCAGTGAATCTACAG 960

QY 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATGGTTGG 1020
DB 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATGGTTGG 1020

QY 1021 ATCAGGATTCAGTTTTCAGATCAGTTTGTAGTGAATTTGAAGTGAATCTCTCGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTTCAGATCAGTTTGTAGTGAATTTGAAGTGAATCTCTCGACTCAG 1080

QY 1081 AAGATTATAGCCCTTGTGAAGGACAAAGACCTCTCAGATGAAGATGATGAGGTATATC 1140
DB 1081 AAGATTATAGCCCTTGTGAAGGACAAAGACCTCTCAGATGAAGATGATGAGGTATATC 1140

QY 1141 AAGTTACTGTGTATCAGGCGGGGAGGTGATACAGATTCATTTGAAGAGATTCCTGAAA 1200
DB 1141 AAGTTACTGTGTATCAGGCGGGGAGGTGATACAGATTCATTTGAAGAGATTCCTGAAA 1200

QY 1201 TTTCTCTAGCTGACTATTTGGAAATGCACTTCATCAATGAATGAATCCCCCTTCCAT 1260
DB 1201 TTTCTCTAGCTGACTATTTGGAAATGCACTTCATCAATGAATGAATCCCCCTTCCAT 1260

QY 1261 CACATTTGCAACAGATGTTGGGCCCTTCTGAGAAATGGCTTCTCTGAAGATAAAGGAAAG 1320
DB 1261 CACATTTGCAACAGATGTTGGGCCCTTCTGAGAAATGGCTTCTCTGAAGATAAAGGAAAG 1320

QY 1321 ATAAAGGGAAATCTCTGAGAAAGCAAACTGGAAGAACTCAACACAGCTGAAGAGGCT 1380
DB 1321 ATAAAGGGAAATCTCTGAGAAAGCAAACTGGAAGAACTCAACACAGCTGAAGAGGCT 1380

QY 1381 TTGATGTTCTGATTTGTAATAAATACTATGATGAATGATTCAGAGAGTCAATGTGTTGAG 1440
DB 1381 TTGATGTTCTGATTTGTAATAAATACTATGATGAATGATTCAGAGAGTCAATGTGTTGAG 1440

QY 1441 AAAATGATGATAAATACTACAAAGCTTCACAAATCACAAGAAAGTGAAGACTATTTTCAGC 1500
DB 1441 AAAATGATGATAAATACTACAAAGCTTCACAAATCACAAGAAAGTGAAGACTATTTTCAGC 1500

QY 1501 CATCAACTTCTAGTAGCATTATTTATAGCAGCAAGAGATGTAAGAGTGAAGAGG 1560
DB 1501 CATCAACTTCTAGTAGCATTATTTATAGCAGCAAGAGATGTAAGAGTGAAGAGG 1560

QY 1561 AAGAAACCAAGCAAGAAAGAGAGTGGAAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
DB 1561 AAGAAACCAAGCAAGAAAGAGAGTGGAAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620

QY 1621 CTGTGTGATTTGTCAAGTGCACCTAAAATGTTGCAATTTCCATTTGCCATGAAGAGAC 1680
DB 1621 CTGTGTGATTTGTCAAGTGCACCTAAAATGTTGCAATTTGCCATGAAGAGAC 1680

QY 1681 ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAAGAAAGAAATAGCCCTGCCAG 1740
DB 1681 ATCTTATGGCTGCTTTACATGTGCAAAAGAGCTTAAAGAAAGAAATAGCCCTGCCAG 1740

QY 1741 TATGTAGAACCAATTCAAATGATTTGCTAACTTATTTCCCTAGTTCACCTGTCTAT 1800
DB 1741 TATGTAGAACCAATTCAAATGATTTGCTAACTTATTTCCCTAGTTCACCTGTCTAT 1800

QY 1801 AAGAGATTTATATATTTTAACTATATAACCTTAGGAATTTAGACAACTGAAATTTAT 1860
DB 1801 AAGAGATTTATATATTTTAACTATATAACCTTAGGAATTTAGACAACTGAAATTTAT 1860

QY 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTTTAGTATAT 1920
DB 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATAGATTTCTCTTTAGTATAT 1920

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| | | | |
|----|------|---|------|
| QY | 1921 | TGACCTACTTTGGTAGTGGGAATAGTAATCTACTATAATTTGGACTTGAATATGTAGCT | 1980 |
| Db | 1921 | TGACCTACTTTGGTAGTGGGAATAGTGAATCTACTATAATTTGGACTTGAATATGTAGCT | 1980 |
| QY | 1981 | CATCCCTTTACACCAACTCTCTAAATTTAAATAAATTTCTACTCTGTCTTAAATGAGAAGTAC | 2040 |
| Db | 1981 | CATCCCTTTACACCAACTCTCTAAATTTAAATAAATTTCTACTCTGTCTTAAATGAGAAGTAC | 2040 |
| QY | 2041 | TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTATATTTTTTTTG | 2100 |
| Db | 2041 | TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACCTTATATTTTTTTTG | 2100 |
| QY | 2101 | AGACCGAGTCTTGCTCTGTATCCACGAGCTGAGTGCAGTGGGTGATCTTGSCCTCACTGCA | 2160 |
| Db | 2101 | AGACCGAGTCTTGCTCTGTATCCACGAGCTGAGTGCAGTGGGTGATCTTGSCCTCACTGCA | 2160 |
| QY | 2161 | AGCTCTGCCCTCCCGGGTTGCGACCATCTTCCTGCCCTCAGCCCTCCCAATTTAGCTTGGCC | 2220 |
| Db | 2161 | AGCTCTGCCCTCCCGGGTTGCGACCATCTTCCTGCCCTCAGCCCTCCCAATTTAGCTTGGCC | 2220 |
| QY | 2221 | TACAGTCATCTGCCACACACACTCGGCTAAATTTTTTTGTACTTTTTTAGTAGAGACAGGGTTTC | 2280 |
| Db | 2221 | TACAGTCATCTGCCACACACACTCGGCTAAATTTTTTTGTACTTTTTTAGTAGAGACAGGGTTTC | 2280 |
| QY | 2281 | ACCGTGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTTCGSCCTCC | 2340 |
| Db | 2281 | ACCGTGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCCACCTTCGSCCTCC | 2340 |
| QY | 2341 | CAAGTGTCTGGGATTTACAGCATAGGCCACCG | 2372 |
| Db | 2341 | CAAGTGTCTGGGATTTACAGCATAGGCCACCG | 2372 |

RESULT 4

US-08-245-500A-2

; Sequence 2, Application US/08245500A

; Patent No. 5550023

; GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE

APPLICANT: HILL, DAVID E.

APPLICANT: KINZLER, KENNETH W.

APPLICANT: VOGELSTEIN, BERT

; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

; TITLE OF INVENTION: HUMAN TUMOR

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G STREET, N.W.

; CITY: WASHINGTON

STATE: D.C.

; COUNTRY: USA

; ZIP: 20001

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/245,500A

;
FILING DATE: 07-APR-1993

; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A

; REGISTRATION NUMBER: 32,141

;
; REFERENCE/DOCKET NUMBER: 01107.42798

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-910

TELEFAX: 202-508-9299

; TELEX: 197430 BBMB UT

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2372 base p

; TYPE: nucleic acid

| | | |
|--|---------------------|--|
| : | STRANDEDNESS: | double |
| : | TOPOLOGY: | linear |
| : | MOLECULE TYPE: | cdna |
| : | HYPOTHETICAL: | NO |
| : | ANTI-SENSE: | NO |
| : | ORIGINAL SOURCE: | |
| : | ORGANISM: | Homo sapiens |
| : | CELL LINE: | Caco-2 |
| : | POSITION IN GENOME: | |
| : | MAP POSITION: | 12q12-14 |
| : | FEATURE: | |
| : | NAME/KEY: | CDS |
| : | LOCATION: | 312..1784 |
| : | US-08-245-500A-2 | |
| Query Watch 100.0%; Score 2372; DB 1; Length 2372; | | |
| Best Local Similarity 100.0%; Pred. No. 0; | | |
| Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 9 | | |
| Qy | 1 | GCACCGCGGAGCTTGGCTGCTTTGTGGGCCCTGTGTGGCCCTGTGTGCGAAAGATGGA |
| Db | 1 | GCACCGCGGAGCTTGGCTGCTTCGTGGGCCCTGTGTGGCCCTGTGTGCGAAAGATGGA |
| Qy | 61 | GCAGAAGCCGAGCCGAGGGGGCGCGACCCTCTGTACCGAGATCCTTGCTGCTTTGC |
| Db | 61 | GCNAGAACCCGAGCCGAGGGGGCGCGACCCCTCTGACCGAGATCCTTGCTGCTTTGC |
| Qy | 121 | CAGCCAGGAGCACCGTCCCTCCCCGGGANTAGTGCGTACAGGCGCCAGTGCCTTGGCCCG |
| Db | 121 | CAGCCAGGAGCACCGTCCCTCCCCGGATTAGTGCSTFACGAGCGCCAGTGCCTTGGCCCG |
| Qy | 181 | GAGAGTGGAAATGATCCC CGAGGCCAGGGCGCTCGTCTTCGCGCATGTCAGTCCCGGTG |
| Db | 181 | GAGAGTGGAAATGATCCC CGAGGCCAGGGCGCTCGTCTTCGCGCATGTCAGTCCCGGTG |
| Qy | 241 | AAGGAACCTGGGGAGCTTTGAGGAGCCCCCGACTCCAGCGCGAAAACCCCGATGGTGA |
| Db | 241 | AAGGAACCTGGGGAGCTTTGAGGAGCCCCCGACTCCAGCGCGAAAACCCCGATGGTGA |
| Qy | 301 | GGAGCAGGCAAAATGTGCAATACCAAATGTCTGTACTCTACTGATGGTCTGTAAACCACT |
| Db | 301 | GGAGCAGGCAAAATGTGCAATACCAAATGTCTGTACTCTACTGATGGTCTGTAAACCACT |
| Qy | 361 | CACAGATTCCAGCTTCGGAACAAGAGACCTGGTAGACCAAGCCATGCTTTTGAAGT |
| Db | 361 | CACAGATTCCAGCTTCGGAACAAGAGACCTGGTAGACCAAGCCATGCTTTTGAAGT |
| Qy | 421 | TATTAAAGTCTTTGGTGCAAAAAAGACACTTATACTATGAAGAGAGTCTTTTTATC |
| Db | 421 | TATTAAAGTCTTTGGTGCAAAAAAGACACTTATACTATGAAGAGAGTCTTTTTATC |
| Qy | 481 | TTGGCCAGTATATTATGACTTAACGATTATATCATCAGAGCAACAACATATTCATATT |
| Db | 481 | TTGGCCAGTATATTATGACTTAACGATTATATCATCAGAGCAACAACATATTCATATT |
| Qy | 541 | GTTCAAATGATCTCTAGGAGATTGTTTGGCGTGCCAAGCTTCTCTGTGAAGAGAGCACA |
| Db | 541 | GTTCAAATGATCTCTAGGAGATTGTTTGGCGTGCCAAGCTTCTCTGTGAAGAGAGCACA |
| Qy | 601 | GGAAATATATACCATGATCTACAGGAACCTTGSTAGTACTCAATCAGCAGAAATCATCGG |
| Db | 601 | GGAAATATATACCATGATCTACAGGAACCTTGSTAGTACTCAATCAGCAGAAATCATCGG |
| Qy | 661 | ACTCAGGTACATCTCTGAGTGAGAACAGGTGTCACTTCAAGGTGGGAGTATCAAAAGG |
| Db | 661 | ACTCAGGTACATCTCTGAGTGAGAACAGGTGTCACTTCAAGGTGGGAGTATCAAAAGG |
| Qy | 721 | ACCTTGTACACAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTCTTAGACCAT |
| Db | 721 | ACCTTGTACACAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTCTTAGACCAT |
| Qy | 781 | CTACCTCATCTTAGAAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATTTCTG |
| Db | 781 | CTACCTCATCTTAGAAGGAGAGCAATTAGTGAGACAGAGAAATTCAGATGAATTTCTG |

Db 781 CTACCTCATCTAGAGGAGAGCAATTAGTGAGACAGAGAAAATTCAGATGAATATCTG 840
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Db 841 GTCAAGCACAAGAAACCCACAATCTGATAGTATTTCCCTTTGATGAAGCC 900
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Db 901 TGGCTCTGTGTATAGGGAGATATCTTGTGAAGAACGAGTACGAGTGAATCTACAG 960
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Db 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATGGTTGG 1020
Qy 1021 ATCAGATTCAGTTCAGATCATCTGATGCTGGTGAAGTGAACATTCAGGTGATGGTTGG 1080
Db 1021 ATCAGATTCAGTTCAGATCATCTGATGCTGGTGAAGTGAACATTCAGGTGATGGTTGG 1080
Qy 1081 AAGATTATAGCCTTAGTGAAGAACGACAACTCTCAGATGAAGATGATGAGGTATATC 1140
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Db 1141 AAGTTACTGTGTATCAGGAGGAGAGTATACAGATTCATTTGAAGAAAGATCCCTGAAA 1200
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Qy 1261 CACATTGCAACAGATTTGGGCCCTTCGTGAGAAATTTGGCTTCCCTGAAGATTAAGGGGAAAG 1320
Db 1261 CACATTGCAACAGATTTGGGCCCTTCGTGAGAAATTTGGCTTCCCTGAAGATTAAGGGGAAAG 1320
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Db 1321 ATAAAGGGAAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAGCTGAAGAGGGCT 1380
Qy 1381 TTGATGTTCTGATTTGAAAAAATCTAGTGAATGATTCAGAGATCATGTGTTGAGG 1440
Db 1381 TTGATGTTCTGATTTGAAAAAATCTAGTGAATGATTCAGAGATCATGTGTTGAGG 1440
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Db 1441 AAAATGATGATAAAATCACAGCTTCACATCACAGAAAGTGAAGACTATTTCTCAGC 1500
Qy 1501 CATCACTTCTAGTACATTTATAGCAGCCAGAGATGTCAGAGCTTGAAGAGG 1560
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Db 1561 AAGAAACCCAGACAAAGAGAGTGTGGAATCTAGTTTCCCTTTAATGCCATTGAAC 1620
Qy 1621 CTTGTGTGATTTGTCAGGTGACCTTAAATGTTGATTCATGTCGCAAAACAGGAC 1680
Db 1621 CTTGTGTGATTTGTCAGGTGACCTTAAATGTTGATTCATGTCGCAAAACAGGAC 1680
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Db 1681 ATCTTATGGCTGCTTTACATGTGCAAGAACCTAAAGAAAGAAATGAGCCCTGCCAG 1740
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Db 1741 TATGTAGACACCAATTCATGATTTGCTAACTTATTTCCCTTAGTTGACCTGTCTAT 1800
Qy 1801 AAGAGATTTATATTTCTAATCATATATACCTAGATTTAGACAACTGGAATTTAT 1860
Db 1801 AAGAGATTTATATTTCTAATCATATATACCTAGATTTAGACAACTGGAATTTAT 1860
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Db 1861 CACATATATCAAGTGAAGAAATGCTCAATTCACATGATTTCTTCTTTAGTATAAT 1920

Qy 1921 TGACCTACTTTGGTAGTGAATAGTGAATCTTACTATATAATTGACTTGAATATGAGCT 1980
Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATCTTACTATATAATTGACTTGAATATGAGCT 1980
Qy 1981 CATCTTTTACACCACTCTTAATTTAAATTTTCTACTCTGTCTTAAATGAGAAGTAC 2040
Db 1981 CATCTTTTACACCACTCTTAATTTAAATTTTCTACTCTGTCTTAAATGAGAAGTAC 2040
Qy 2041 TTGGTTTTTTTTTCTTAAATATATATGACATTTAAATGTAACATTAATTTTTTTT 2100
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Qy 2161 AGCTTGCCCTCCCGGGTTCGGACCATTCCTCTGCTCAGCTCCCATTTAGCTTGCC 2220
Db 2161 AGCTTGCCCTCCCGGGTTCGGACCATTCCTCTGCTCAGCTCCCATTTAGCTTGCC 2220
Qy 2221 TACAGTCTATCTGCCACCACTGCTGCTAAATTTTGTACTTTTGTAGAGACAGGTTTC 2280
Db 2221 TACAGTCTATCTGCCACCACTGCTGCTAAATTTTGTACTTTTGTAGAGACAGGTTTC 2280
Qy 2281 ACCGTGTTAGCAGGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTCGSCCTCC 2340
Db 2281 ACCGTGTTAGCAGGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTCGSCCTCC 2340
Qy 2341 CAAAGTGTGGATTACAGGATGAGCCAGC 2372
Db 2341 CAAAGTGTGGATTACAGGATGAGCCAGC 2372

RESULT 5
US-08-390-546-2
; Sequence 2. Application US/08390546
; Patent No. 5606044
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,546
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: CaCo-2
; POSITION IN GENOME:
; MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
; US-08-390-546-2

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Query Match          100.0%  Score 2372;  DB 1;  Length 2372;
Best Local Similarity 100.0%  Pred. No. 0;
Matches 2372;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy 1 GCACCGCGGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGTCGGAAGATGGA 60
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Qy 121 CAGCAGGAGGACCGTCCCTCCCGGATAGTGGGTAGGAGCGGCCAGTGCCTGCCCGCG 180
Db 121 CAGCAGGAGGACCGTCCCTCCCGGATAGTGGGTAGGAGCGGCCAGTGCCTGCCCGCG 180

Qy 181 GAGAGTGGAAATATCCCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
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Qy 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACCTACTGATGTGTGTGTGTGTGTGT 360
Db 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACCTACTGATGTGTGTGTGTGTGTGT 360

Qy 361 CACAGATTCAGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 361 CACAGATTCAGCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420

Qy 421 TATTAAGTCTGTGTGTGCACAAAGACACTTATCTATGATGAGGAGGAGGAGGAGGAGGAG 480
Db 421 TATTAAGTCTGTGTGTGCACAAAGACACTTATCTATGATGAGGAGGAGGAGGAGGAGGAG 480

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Db 481 TTGGCCAGTATATATGACTTAACGATATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 540

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Qy 781 CTACCTCACTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840

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Db 841 GTGAAGCACAAGAAAGAAAGCCCAAAATCTGATAGTATTTCCCTTTCTCTTGTGTAAGCC 900
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Qy 1861 CACATATATCAAGAGTCAGAAATGCTCAATTCATAGATTTCTTCTCTTTAGTATAT 1920

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Db 1861 CACATATATCAAAAGTGAGAAATGCTCAATTCACATAGATTCTCTCTTTAGTATAAT 1920
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Qy 2041 TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATTAATTAATTTTGTG 2100
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Db 2341 CAAAGTCTGGGATTCAGCGGATGAGCCACCG 2372

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RESULT 6

US-08-390-479A-2

Sequence 2, Application US/08390479A

Patent No. 5618921

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE

APPLICANT: HILL, DAVID E.

APPLICANT: KINZLER, KENNETH W.

APPLICANT: VOGELSTEIN, BERT

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDW2 GENE IN

TITLE OF INVENTION: HUMAN TUMORS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER & WITCOFF, LTD.

STREET: 1001 G STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/390,479A

FILING DATE: 02-FEB-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.48992

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

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; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Homo sapiens
; CELL LINE: CaCo-2
; POSITION IN GENOME:
; MAP POSITION: 12q12-14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 312..1784
; US-08-390-479A-2

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Query Match      100.0%; Score 2372; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GCAAGAAAGCGAGCGCGCGCGCGCGCGCGCTCTGACCGAGATCCTGCTGCTTCG 120
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Db 421 TATTAAAGTCTGTGGTGCACAAAAGACACTTATATGAAAGAGGTCTCTTTTATC 480
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Db 721 ACCTTGTAAGAGCTTCAGGAAAGAAACCTTTCATCTTTACATTTGGTTTCTAGACCAT 780

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QY 781 CTACCTCATCTAGAGGAGCAATAGTGAGACAGAGAAATTCAGATGATATCTG 840
 Db 781 CTACCTCATCTAGAGGAGCAATAGTGAGACAGAGAAATTCAGATGATATCTG 840
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 Db 841 GTGACGCAAGAAAGCCACAAATCTCATAGTATTCCTTTCCCTTTGATGAAGCC 900
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 Db 901 TGGCTCTGTGTAAATAGGAGAGATGTTGTGAAGAGAGAGAGAGAGAGAGAG 960
 QY 961 GGAGCCATCAATCCGATCTTGATGCTGGTGAAGTGAATTCAGTGAATGGTTGG 1020
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 QY 1021 ATCAGGATTCAGTTTCAGATCAGTTAGTGTAGAATTTGAAAGTTCCTCGACTCAG 1080
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 QY 1081 AAGATTATAGCCTTAGTCAAGAGAGCAAGAACTCTCAGATGAAGATGATGATATC 1140
 Db 1081 AAGATTATAGCCTTAGTCAAGAGAGCAAGAACTCTCAGATGAAGATGATGATATC 1140
 QY 1141 AAGTTACTGTGTATCAGGAGAGAGAGATGATACAGATTCATTTGAAGAGATCCTGAAA 1200
 Db 1141 AAGTTACTGTGTATCAGGAGAGAGAGATGATACAGATTCATTTGAAGAGATCCTGAAA 1200
 QY 1201 TTTCTTAGCTAGCTATGGAATGCACTTCATGCAATGAATGAATCCGCCCTTCCAT 1260
 Db 1201 TTTCTTAGCTAGCTATGGAATGCACTTCATGCAATGAATGAATCCGCCCTTCCAT 1260
 QY 1261 CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCTGAAAGATAAGGAAAAG 1320
 Db 1261 CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCTGAAAGATAAGGAAAAG 1320
 QY 1321 ATAAGGGGAATCTGAGAAAGCCAACTGAAACTCAACACAGCTGAAGGGCT 1380
 Db 1321 ATAAGGGGAATCTGAGAAAGCCAACTGAAACTCAACACAGCTGAAGGGCT 1380
 QY 1381 TTGATGTTCCCTGATTTAAAAAACTATAGTGAATGATTTCCAGAGATCATGTTGAGG 1440
 Db 1381 TTGATGTTCCCTGATTTAAAAAACTATAGTGAATGATTTCCAGAGATCATGTTGAGG 1440
 QY 1441 AAAATGATGATAAATACCAAGCTTCACATCAAGAAAGTGAAGACTATCTCAGC 1500
 Db 1441 AAAATGATGATAAATACCAAGCTTCACATCAAGAAAGTGAAGACTATCTCAGC 1500
 QY 1501 CATCAACTCTAGTAGCATTATTTATAGCAGCAAGAGATGTAAGAGTTTGAAGGG 1560
 Db 1501 CATCAACTCTAGTAGCATTATTTATAGCAGCAAGAGATGTAAGAGTTTGAAGGG 1560
 QY 1561 AAGAACCCAGCAAGAGAGAGAGTGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
 Db 1561 AAGAACCCAGCAAGAGAGAGAGTGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
 QY 1621 CTTGTGATTTGTCAAGGTCGACCTAAAAATGTTTGCATTGTCCATGTCACAAACAGGAC 1680
 Db 1621 CTTGTGATTTGTCAAGGTCGACCTAAAAATGTTTGCATTGTCCATGTCACAAACAGGAC 1680
 QY 1681 ATCTATGCTGCTTTACATGTGCAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1740
 Db 1681 ATCTATGCTGCTTTACATGTGCAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1740
 QY 1741 TATGTAGCAACCAATTCATGCTGCTAACTTATTTCCCTAGTTGACCTGCTCAT 1800
 Db 1741 TATGTAGCAACCAATTCATGCTGCTAACTTATTTCCCTAGTTGACCTGCTCAT 1800
 QY 1801 AAGAGAAATTTATTTCTAATCTATATACCTTAGCAATTTAGACAACTGAAATTTAT 1860
 Db 1801 AAGAGAAATTTATTTCTAATCTATATACCTTAGCAATTTAGACAACTGAAATTTAT 1860
 QY 1861 CACATATACAAAGTGAGAAATGCCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920

Db 1861 CACATATACAAAGTGAGAAATGCCTCAATTCACATAGATTTCTTCTTTAGTATAAT 1920
 QY 1921 TGACCTTACTTTGGTAGTGAATAGTGAATAGTGAATAGTGAATAGTGAATAGTGAATAGTGA 1980
 Db 1921 TGACCTTACTTTGGTAGTGAATAGTGAATAGTGAATAGTGAATAGTGAATAGTGAATAGTGA 1980
 QY 1981 CATCCTTTACACCAACTCCTAAATTTAAATTAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 Db 1981 CATCCTTTACACCAACTCCTAAATTTAAATTAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
 QY 2041 TTGGTTTTTTTCTTAAATATGATATGACATTTAAATGTAATATTTATTTTGG 2100
 Db 2041 TTGGTTTTTTTCTTAAATATGATATGACATTTAAATGTAATATTTATTTTGG 2100
 QY 2101 AGACCGAGTCTTGGCTCTTACCAGGCTGGAGTGGAGTGGCTGATCTTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTTGGCTCTTACCAGGCTGGAGTGGAGTGGCTGATCTTGGCTCACTGCA 2160
 QY 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCTCAGCCTCCCAATTAGCTTTGGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCTCAGCCTCCCAATTAGCTTTGGCC 2220
 QY 2221 TACAGTCTATCTCCACACACACTGCTAAATTTTGTACTTTTAGTAGACAGAGGTTTC 2280
 Db 2221 TACAGTCTATCTCCACACACACTGCTAAATTTTGTACTTTTAGTAGACAGAGGTTTC 2280
 QY 2281 ACCGTGTTAGCAGAGATGCTCGATCTCCTGACCTGATCGGCCACCTCGGCTCC 2340
 Db 2281 ACCGTGTTAGCAGAGATGCTCGATCTCCTGACCTGATCGGCCACCTCGGCTCC 2340
 QY 2341 CAAAGTCTGGGATTACAGGATGAGCCACCG 2372
 Db 2341 CAAAGTCTGGGATTACAGGATGAGCCACCG 2372

RESULT 7
 US-08-557-393-2
 ; Sequence 2, Application US/08557393
 ; Patent No. 5702903
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; APPLICANT: HILL, DAVID E.
 ; APPLICANT: KINZLER, KENNETH W.
 ; APPLICANT: VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/557,393
 ; FILING DATE: 13-NOV-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/245,500
 ; FILING DATE: 18-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAGAN, SARAH A.
 ; REGISTRATION NUMBER: 32,141
 ; REFERENCE/DOCKET NUMBER: 01107.42798
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-508-9100

| | | | | |
|----|------|--------------------------|---|------|
| QY | 721 | ACCTTGTCAGAGCCTT | CAGGAAGAACAACCTTCACTCTTCACATTTGGTTTCTAGACCAT | 780 |
| | | | | |
| Db | 721 | ACCTTGTACAGAGCTTC | CAGGAAGAACAACCTTCATCTTCACATTTGGTTTCTAGACCAT | 780 |
| | | | | |
| QY | 781 | CTACTCATCTAGAAGGAGCAATT | TAGTGAGACAGAAGAAAATTCCAGATGAATTAATCTG | 840 |
| | | | | |
| Db | 781 | CTACTCATCTAGAAGGAGCAATT | TAGTGAGACAGAAGAAAATTCCAGATGAATTAATCTG | 840 |
| | | | | |
| QY | 841 | GTAACGACAAAGAAACCCACAANT | CTGATAGTATTTCCCTTTCTTCATGCATAAGGCC | 900 |
| | | | | |
| Db | 841 | GTAACGACAAAGAAACCCACAANT | CTGATAGTATTTCCCTTTCTTCATGCATAAGGCC | 900 |
| | | | | |
| QY | 901 | TGGCTCTGTGTGTAA | TAAAGGGAGATNGTGTGAAGACGAGTAGCAGTGAATCTCACAG | 960 |
| | | | | |
| Db | 901 | TGGCTCTGTGTGTAA | TAAAGGGAGATNGTGTGAAGACGAGTAGCAGTGAATCTCACAG | 960 |
| | | | | |
| QY | 961 | GGACGCCATCGAATCCGGATCTT | GATGCTGGTGTAAAGCAATTCAGGTGATTTGGTGTG | 1020 |
| | | | | |
| Db | 961 | GGACGCCATCGAATCCGGATCTT | GATGCTGGTGTAAAGCAATTCAGGTGATTTGGTGTG | 1020 |
| | | | | |
| QY | 1021 | ATCAGGATTCAGTTTT | CAGATCAGTTTTAGTGTAGAAATTTCAAGTTCAATCTCTCGACTCAC | 1080 |
| | | | | |
| Db | 1021 | ATCAGGATTCAGTTTT | CAGATCAGTTTTAGTGTAGAAATTTCAAGTTCAATCTCTCGACTCAC | 1080 |
| | | | | |
| QY | 1081 | AGATTTATGCCCTTAGTGAAG | ACAGCAAGCACTCCAGATGAATGATCAGTGAATGATCAGGTATATC | 1140 |
| | | | | |
| Db | 1081 | AGATTTATGCCCTTAGTGAAG | ACAGCAAGCACTCCAGATGAATGATCAGTGAATGATCAGGTATATC | 1140 |
| | | | | |
| QY | 1141 | AAGTTACTGTGTATCAGG | CAGGGGAGTGATCAGATTCATTTGAAGAAGATCCTGAAA | 1200 |
| | | | | |
| Db | 1141 | AAGTTACTGTGTATCAGG | CAGGGGAGTGATCAGATTCATTTGAAGAAGATCCTGAAA | 1200 |
| | | | | |
| QY | 1201 | TTTCCCTTAGCTGACTATT | TGAAAAATGCATTCATGCAATGAATGAATCCCCCCTTCCAT | 1260 |
| | | | | |
| Db | 1201 | TTTCCCTTAGCTGACTATT | TGAAAAATGCATTCATGCAATGAATGAATCCCCCCTTCCAT | 1260 |
| | | | | |
| QY | 1261 | CACATTGACACAGATGT | TGGGCCCTTCGTGAGATTTGGCTCCTGAGNTAAGSGAAG | 1320 |
| | | | | |
| Db | 1261 | CACATTGACACAGATGT | TGGGCCCTTCGTGAGATTTGGCTCCTGAGNTAAGSGAAG | 1320 |
| | | | | |
| QY | 1321 | ATAAAGGGAAATCTCT | GAGAAGCCAACCTGAGAAAACCTCAACACAGCTGAAGAGGCT | 1380 |
| | | | | |
| Db | 1321 | ATAAAGGGAAATCTCT | GAGAAGCCAACCTGAGAAAACCTCAACACAGCTGAAGAGGCT | 1380 |
| | | | | |
| QY | 1381 | TTGATGTTCCCTGATGT | TAAAAAAAATAGTGAATGATTTCCAGAGAGTCATGTCTGAGG | 1440 |
| | | | | |
| Db | 1381 | TTGATGTTCCCTGATGT | TAAAAAAAATAGTGAATGATTTCCAGAGAGTCATGTCTGAGG | 1440 |
| | | | | |
| QY | 1441 | AAAATGATGATAAATTT | TACACAGCTTCACAATCACAGAAGAGTGAAGACTATTTCTCAGC | 1500 |
| | | | | |
| Db | 1441 | AAAATGATGATAAATTT | TACACAGCTTCACAATCACAGAAGAGTGAAGACTATTTCTCAGC | 1500 |
| | | | | |
| QY | 1501 | CATCAACTTCTAGTAGCNT | ATTTATAGCACCAAGAGATGTGAAGNGTGTGAAGGG | 1560 |
| | | | | |
| Db | 1501 | CATCAACTTCTAGTAGCNT | ATTTATAGCACCAAGAGATGTGAAGNGTGTGAAGGG | 1560 |
| | | | | |
| QY | 1561 | AAGAAACCCACAGACA | AAAGAGAGTGTGGAATCTAGTTTGGCCCCCTTAATGCCATTTGAAC | 1620 |
| | | | | |
| Db | 1561 | AAGAAACCCACAGACA | AAAGAGAGTGTGGAATCTAGTTTGGCCCCCTTAATGCCATTTGAAC | 1620 |
| | | | | |
| QY | 1621 | CTTGTGTGATTTGT | TCAAGGTCGACCTTAAAAATGGTTGCATTTGCTCCATGSCAAAACAGAC | 1680 |
| | | | | |
| Db | 1621 | CTTGTGTGATTTGT | TCAAGGTCGACCTTAAAAATGGTTGCATTTGCTCCATGSCAAAACAGAC | 1680 |
| | | | | |
| QY | 1681 | ATCTTATGGCTGCTTT | TACATGTGCAAGAGAGCTTAAGAAAAGGATAGGCCCTGCCAC | 1740 |
| | | | | |
| Db | 1681 | ATCTTATGGCTGCTTT | TACATGTGCAAGAGAGCTTAAGAAAAGGATAGGCCCTGCCAC | 1740 |
| | | | | |
| QY | 1741 | TATGTAGACAACCAAT | TTCAAATGATTTGCTAACCTATTTTCCCCTAGTTGACCTGTCTAT | 1800 |
| | | | | |
| Db | 1741 | TATGTAGACAACCAAT | TTCAAATGATTTGCTAACCTATTTTCCCCTAGTTGACCTGTCTAT | 1800 |
| | | | | |

RESULT 9

RESULT 9
US-08-390-517A-2

US-08-390-51/A-2
: sequence 2 Application US/08390517A

: Sequence 2, Applicant
: Patent No. 5736338

Patent No. 5736338

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE

APPLICANT: HILL, DAVID E.

APPLICANT: KINZLER, KENNETH

APPLICANT: VOGELSTEIN, BERT

; TITLE OF INVENTION: AMPLIFICATION

TITLE OF INVENTION: HU

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

CORRESPONDENCE: B
; ADDRESSEE: B

;
; ADDRESS: B
; STREET: 1001

STREET: WASH
CITY: WASH

;
CITY: WASHINGTON
STATE: D C

STATE: D.C.
COUNTRY: USA

COUNTRY: USA
ZID: 20001

; ZIP: 20001
; COMPUTER RESEARCH FORM:

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy di

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/

SOFTWARE: PatentIn R

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: U

AFFILIATION NUMBER: 03/00/3
 FILING DATE: 07-APR-1993

FILED DATE: 07-APR-1993
CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 197430 BBMB UT
 INFORMATION FOR SEO ID NO. 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL LINE: CaCo-2
 POSITION IN GENOME:
 MAP POSITION: 12q12-14
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 312..1784
 US-08-390-517A-2

Query Match 100.0%; Score 2372; DB 1; Length 2372;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|-----------------------------|-----|
| Qy | 1 | GCACCGCGGAGCTGGCTGCTCTGCGG | 60 |
| Db | 1 | GCACCGCGGAGCTGGCTGCTCTGCGG | 60 |
| Qy | 61 | GCAAGAACGCGAGCGCGGCGGCGGCGG | 120 |
| Db | 61 | GCAAGAACGCGAGCGCGGCGGCGGCGG | 120 |
| Qy | 121 | CAGCAGGAGCAGCTGCTCCCGGATTA | 180 |
| Db | 121 | CAGCAGGAGCAGCTGCTCCCGGATTA | 180 |
| Qy | 181 | GAGAGTGAATGATCCCGAGCGCCAGG | 240 |
| Db | 181 | GAGAGTGAATGATCCCGAGCGCCAGG | 240 |
| Qy | 241 | AAGGAACTGGGAGCTTTGAGGACCC | 300 |
| Db | 241 | AAGGAACTGGGAGCTTTGAGGACCC | 300 |
| Qy | 301 | GGAGCAGGCAATGTCATACCAACAT | 360 |
| Db | 301 | GGAGCAGGCAATGTCATACCAACAT | 360 |
| Qy | 361 | CACAGATTCCAGCTTCCGAAACAG | 420 |
| Db | 361 | CACAGATTCCAGCTTCCGAAACAG | 420 |
| Qy | 421 | TATTAAAGTCTGTTGGTGCACAAA | 480 |
| Db | 421 | TATTAAAGTCTGTTGGTGCACAAA | 480 |
| Qy | 481 | TGGCCAGTATATATGACTAAACG | 540 |
| Db | 481 | TGGCCAGTATATATGACTAAACG | 540 |
| Qy | 541 | GTTCAAAATGATCTCTAGGAGATT | 600 |
| Db | 541 | GTTCAAAATGATCTCTAGGAGATT | 600 |
| Qy | 601 | GGAAATATATACCATGATCTACG | 660 |
| Db | 601 | GGAAATATATACCATGATCTACG | 660 |
| Qy | 661 | ACTCAGGTACATCTGTGAGTGAG | 720 |
| Db | 661 | ACTCAGGTACATCTGTGAGTGAG | 720 |

| | | | |
|----|------|-------------------------|------|
| Db | 661 | ACTCAGGTACATCTGTGAGTGAG | 720 |
| Qy | 721 | ACCTTGACAAAGAGCTTACAGG | 780 |
| Db | 721 | ACCTTGACAAAGAGCTTACAGG | 780 |
| Qy | 781 | CTACCTCATCTAGAGGAGCAAT | 840 |
| Db | 781 | CTACCTCATCTAGAGGAGCAAT | 840 |
| Qy | 841 | GTGAACGACAAAGAAACGCCA | 900 |
| Db | 841 | GTGAACGACAAAGAAACGCCA | 900 |
| Qy | 901 | TGGCTCTGTGTAATAAGGAGAT | 960 |
| Db | 901 | TGGCTCTGTGTAATAAGGAGAT | 960 |
| Qy | 961 | GGACGCATCGAATCCGGATCT | 1020 |
| Db | 961 | GGACGCATCGAATCCGGATCT | 1020 |
| Qy | 1021 | ATCAGGATTCAGTTTCAGATCA | 1080 |
| Db | 1021 | ATCAGGATTCAGTTTCAGATCA | 1080 |
| Qy | 1081 | AAGATTATACCTTACTGAGG | 1140 |
| Db | 1081 | AAGATTATACCTTACTGAGG | 1140 |
| Qy | 1141 | AAGTTACTGTGTATCAGGCGG | 1200 |
| Db | 1141 | AAGTTACTGTGTATCAGGCGG | 1200 |
| Qy | 1201 | TTTCCTTAGCTGACTATTCGAA | 1260 |
| Db | 1201 | TTTCCTTAGCTGACTATTCGAA | 1260 |
| Qy | 1261 | CACATTGCACACAGATGTGGG | 1320 |
| Db | 1261 | CACATTGCACACAGATGTGGG | 1320 |
| Qy | 1321 | ATAAGGGGAAATCTCTGAGA | 1380 |
| Db | 1321 | ATAAGGGGAAATCTCTGAGA | 1380 |
| Qy | 1381 | TTGATGTTCTCTGATTTGTA | 1440 |
| Db | 1381 | TTGATGTTCTCTGATTTGTA | 1440 |
| Qy | 1441 | AAATGATGATAAAATACACA | 1500 |
| Db | 1441 | AAATGATGATAAAATACACA | 1500 |
| Qy | 1501 | CATCAACTTCTAGTAGCATT | 1560 |
| Db | 1501 | CATCAACTTCTAGTAGCATT | 1560 |
| Qy | 1561 | AAGAAACCCCAAGACAAAG | 1620 |
| Db | 1561 | AAGAAACCCCAAGACAAAG | 1620 |
| Qy | 1621 | CTTGTGTGATTTGTCAAGG | 1680 |
| Db | 1621 | CTTGTGTGATTTGTCAAGG | 1680 |
| Qy | 1681 | ATCTTATGGCTCTCTTTAC | 1740 |
| Db | 1681 | ATCTTATGGCTCTCTTTAC | 1740 |
| Qy | 1741 | TATGTAGAACCAATTCAAAT | 1800 |
| Db | 1741 | TATGTAGAACCAATTCAAAT | 1800 |

Qy 1801 AAGAGATATATATTTCTAATATATTAACCCCTAGGAATTTAGACAACCTGAAATTTATT 1860
Db 1801 AAGAGATATATATTTCTAATATATTAACCCCTAGGAATTTAGACAACCTGAAATTTATT 1860
Qy 1861 CACATATATCAAAAGTGCAGAAATGCTCAATTTACATAGATTTCTTCTTTAGTATAAT 1920
Db 1861 CACATATATCAAAAGTGCAGAAATGCTCAATTTACATAGATTTCTTCTTTAGTATAAT 1920
Qy 1921 TGACCTACTTTGGTAGTGAATAGTGAATTTACTTACTATATTTGACTTGAATTTAGCT 1980
Db 1921 TGACCTACTTTGGTAGTGAATAGTGAATTTACTTACTATATTTGACTTGAATTTAGCT 1980
Qy 1981 CATCCTTTACACCAACTCCTAATTTTAAATAATTTTACTCTGTCTTAAATGAGAAGTAC 2040
Db 1981 CATCCTTTACACCAACTCCTAATTTTAAATAATTTTACTCTGTCTTAAATGAGAAGTAC 2040
Qy 2041 TTGGTTTCTTTTCTTAAATATATATGACATTTAAATGTAATTTATTTTCTTTTCTG 2100
Db 2041 TTGGTTTCTTTTCTTAAATATATATGACATTTAAATGTAATTTATTTTCTTTTCTG 2100
Qy 2101 AGACCGAGTCTTCTCTGTTTACCAGGCTGGAGTGCAGTGGTGATCTTGGCTCACTGCA 2160
Db 2101 AGACCGAGTCTTCTCTGTTTACCAGGCTGGAGTGCAGTGGTGATCTTGGCTCACTGCA 2160
Qy 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCCCTCAGCCCTCCCAATTTAGCTTGGC 2220
Db 2161 AGCTCTGCCCTCCCGGGTTCCGACCATTTCTCTGCCCTCAGCCCTCCCAATTTAGCTTGGC 2220
Qy 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGTACAGACAGGGTTTC 2280
Db 2221 TACAGTCATCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGTACAGACAGGGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGGATGCTCGATCTCTGACCTCGATCGCCGACCTCGGCTCC 2340
Db 2281 ACCGTGTTAGCCAGGATGCTCGATCTCTGACCTCGATCGCCGACCTCGGCTCC 2340
Qy 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372

RESULT 10
US-08-390-515A-2
: Sequence 2, Application US/08390515A
: Patent No. 5756455
: GENERAL INFORMATION:
: APPLICANT: BURRELL, MARILEE
: APPLICANT: HILL, DAVID E.
: APPLICANT: KINZLER, KENNETH W.
: APPLICANT: VOGELSTEIN, BERT
: TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDW2 GENE IN
: TITLE OF INVENTION: HUMAN TUMORS
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
: STREET: 1001 G STREET, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/390,515A
: FILING DATE: 07-APR-1993
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: KAGAN, SARAH A.
: REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: CaCo-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-390-515A-2
Query Match 100.0% Score 2372; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCACCCGGGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGAAGATGGA 60
Db 1 GCACCCGGGAGCTTGGCTGCTTCTGGGGCCCTGTGTGGCCCTGTGTGCGAAGATGGA 60
Qy 61 GCAAGAAAGCGAGCCGAGGGCGCGCCGACCCCTCTGACCCGAGATCTGCTGCTTTCG 120
Db 61 GCAAGAAAGCGAGCCGAGGGCGCGCCGACCCCTCTGACCCGAGATCTGCTGCTTTCG 120
Qy 121 CAGCCAGGAGCACCCTCCCTCCCGGATTTAGTGGTACGAGCGCCAGTGCCTGGCCCG 180
Db 121 CAGCCAGGAGCACCCTCCCTCCCGGATTTAGTGGTACGAGCGCCAGTGCCTGGCCCG 180
Qy 181 GAGAGTGAATGATATCCCGAGGCGCCGAGGCGCTGCTGCTTCCGCAAGTGTAGTCCCGCTG 240
Db 181 GAGAGTGAATGATATCCCGAGGCGCCGAGGCGCTGCTGCTTCCGCAAGTGTAGTCCCGCTG 240
Qy 241 AAGGAACTGGGAGTCTTGGAGGACCCCGGACCCGACCTCCAGCGCGAAACCCCGATGTTGA 300
Db 241 AAGGAACTGGGAGTCTTGGAGGACCCCGGACCCGACCTCCAGCGCGAAACCCCGATGTTGA 300
Qy 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACCTACTGTGTGCTGTAAACCACT 360
Db 301 GGAGCAGGCAATGTGCAATACCAATGTCTGTACCTACTGTGTGCTGTAAACCACT 360
Qy 361 CACAGATTTCCAGCTTCGGAAACAGAGACCCCTGGTTAGACCAAGCCCATTCCTTTTGAAGT 420
Db 361 CACAGATTTCCAGCTTCGGAAACAGAGACCCCTGGTTAGACCAAGCCCATTCCTTTTGAAGT 420
Qy 421 TATTAAGTCTGTGTGTCACAAAAGACACTATATATGATGAGAAGCAACATATTGTATT 480
Db 421 TATTAAGTCTGTGTGTCACAAAAGACACTATATATGATGAGAAGCAACATATTGTATT 480
Qy 481 TTGGCCAGTATATTATGACTAAACGATTTATGATGAGAAGCAACATATTGTATT 540
Db 481 TTGGCCAGTATATTATGACTAAACGATTTATGATGAGAAGCAACATATTGTATT 540
Qy 541 GTTCAATGATCTTCTAGGAGATTTGTTGGGTCGCCAAGCTTCTCTGTGAAGAGCACA 600
Db 541 GTTCAATGATCTTCTAGGAGATTTGTTGGGTCGCCAAGCTTCTCTGTGAAGAGCACA 600
Qy 601 GGAATATATATACCATCTACAGAACTTGGTAGTGTCAATCAGCAGGAATCATCGG 660
Db 601 GGAATATATATACCATCTACAGAACTTGGTAGTGTCAATCAGCAGGAATCATCGG 660
Qy 661 ACTCAGTACATCTGTGAGTACAGACAGGCTGTACCTTTGAAGGTTGGGAGTATCAAAAG 720

| | | | |
|----|------|--|------|
| Db | 1681 | ATCTTATGGCGCTGCTTACATGTGCAGAGAGAGCTAAAGAAAAGGAATTAAGCCCTGCCAG | 1740 |
| Qy | 1741 | TATGTAGACAACCAATTCAAATGATGTGCTAACTTATTTCCCTTAGTTGACCTGTCTAT | 1800 |
| Db | 1741 | TATGTAGACAACCAATTCAAATGATGTGCTAACTTATTTCCCTTAGTTGACCTGTCTAT | 1800 |
| Qy | 1801 | AAGACAATTATATATTTCTAACTATATAACCCCTAGGAATTTTACACAACCTGAAAATTTATT | 1860 |
| Db | 1801 | AGAGAAATATATATTTCTTACTATATATACCCCTAGGAATTTTACACAACCTGAAATTTATT | 1860 |
| Qy | 1861 | CACATATATCAAGTAGAGAAAATGCGTCAATTCACATAGAAATTTCTTCTCTTTAGTATAAT | 1920 |
| Db | 1861 | CACATATATCAAGTAGAGAAAATGCGTCAATTCACATAGAAATTTCTTCTCTTTAGTATAAT | 1920 |
| Qy | 1921 | TGACCTACTTTGGTGTAGTGAATAGTAGTAATCTACTATATAATTTGACTTCGAATATCTAGCT | 1980 |
| Db | 1921 | TGACCTACTTTGGTGTAGTGAATAGTAGTAATCTACTATATAATTTGACTTCGAATATCTAGCT | 1980 |
| Qy | 1981 | CATCTCTTTACACCACTCTCTAAATTTTAAATAATTTCTACTCTCTCTTAAATGAGAAGTAC | 2040 |
| Db | 1981 | CATCTCTTTACACCACTCTCTAAATTTTAAATAATTTCTACTCTCTCTTAAATGAGAAGTAC | 2040 |
| Qy | 2041 | TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACTTATATTTATTTTTTTTG | 2100 |
| Db | 2041 | TTGGTTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAACTTATATTTATTTTTTTTG | 2100 |
| Qy | 2101 | AGACCGAGCTGTGCTGTGTATCCACGGCTGCAGTGCAGTGGGTGATCTTGGCTCACTGCA | 2160 |
| Db | 2101 | AGACCGAGCTGTGCTGTGTATCCACGGCTGCAGTGCAGTGGGTGATCTTGGCTCACTGCA | 2160 |
| Qy | 2161 | AGCTCTGCCCTCCCGGGTTGCGACCATTCCTCTGCTCAGCCTCCCAATTAGCTTGGCC | 2220 |
| Db | 2161 | AGCTCTGCCCTCCCGGGTTGCGACCATTCCTCTGCTCAGCCTCCCAATTAGCTTGGCC | 2220 |
| Qy | 2221 | TACAGTCACTGTGCCACCACACACTTGGCTAAATTTTGTGTACTTTTAGTAGAGACAGGGTTTC | 2280 |
| Db | 2221 | TACAGTCACTGTGCCACCACACACTTGGCTAAATTTTGTGTACTTTTAGTAGAGACAGGGTTTC | 2280 |
| Qy | 2281 | ACCGTGTAGCCAGGATGGTCTGATCTCTGACTCTGATCCGCCACCTCGGCCCTCC | 2340 |
| Db | 2281 | ACCGTGTGTAGCCAGGATGGTCTGATCTCTGACTCTGATCCGCCACCTCGGCCCTCC | 2340 |
| Qy | 2341 | CAAAGTCTGGGATTACAGGCATGAGCCACCG | 2372 |
| Db | 2341 | CAAAGTCTGGGATTACAGGCATGAGCCACCG | 2372 |

```

RESULT 12
US-09-073-567-1
; Sequence 1, Application US/09073567
; Patent No. 6013786
; GENERAL INFORMATION:
; APPLICANT: Jiaohong Chen
; APPLICANT: Sudhir Agrawal
; APPLICANT: Ruilwen Zhang
; TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073.567
; FILING DATE:
; CLASSIFICATION:

```

| | | | | | | | | | |
|--|-----------------------------------|---|-----|--|--|--|--|--|--|
| ATTORNEY/AGENT INFORMATION: | | | | | | | | | |
| : | NAME: Greenfield, Michael S. | | | | | | | | |
| : | REGISTRATION NUMBER: 37,147 | | | | | | | | |
| : | REFERENCE/DOCKET NUMBER: 98,057-A | | | | | | | | |
| : | TELECOMMUNICATION INFORMATION: | | | | | | | | |
| : | TELEPHONE: (312) 913-0001 | | | | | | | | |
| : | TELEFAX: (312) 913-0002 | | | | | | | | |
| : | INFORMATION FOR SEQ ID NO: 1: | | | | | | | | |
| : | SEQUENCE CHARACTERISTICS: | | | | | | | | |
| : | LENGTH: 2372 base pairs | | | | | | | | |
| : | TYPE: nucleic acid | | | | | | | | |
| : | STRANDEDNESS: both | | | | | | | | |
| : | TOPOLOGY: linear | | | | | | | | |
| : | MOLECULE TYPE: hmdm2 DNA | | | | | | | | |
| : | HYPOTHETICAL: NO | | | | | | | | |
| : | ANTI-SENSE: NO | | | | | | | | |
| : | US-09-073-567-1 | | | | | | | | |
| Query Match 100.0%; Score 2372; DB 3; Length 2372; | | | | | | | | | |
| Best Local Similarity 100.0%; Pred. No. 0; | | | | | | | | | |
| Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps | | | | | | | | | |
| Qy | 1 | GCACCGCGAGCTGGCTGCTTCTGGGCGCTGTGTGGCCCTGTGTGCGCCCTGTGTGCGAAGATGGA | 60 | | | | | | |
| Db | 1 | | | | | | | | |
| Qy | 61 | GCAGAAGCCGAGCCGAGGGCGGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG | 120 | | | | | | |
| Db | 61 | GCAGAAGCCGAGCCGAGGGCGGCGGACCCCTCTGACCGAGATCCTGCTGCTTTCG | 120 | | | | | | |
| Qy | 121 | CAGCCAGGAGCACGCTCCCTCCCGGATTAGTGCGTACGAGCGCCAGTGCCTTGGCCCCG | 180 | | | | | | |
| Db | 121 | CAGCCAGGAGCACGCTCCCTCCCGGATTAGTGCGTACGAGCGCCAGTGCCTTGGCCCCG | 180 | | | | | | |
| Qy | 181 | GAGAGTGAATGATCCCGAGGCGCCAGGGCGTGGTCTTCCGCACTAGTCTAGTCCCGGTG | 240 | | | | | | |
| Db | 181 | GAGAGTGAATGATCCCGAGGCGCCAGGGCGTGGTCTTCCGCACTAGTCTAGTCCCGGTG | 240 | | | | | | |
| Qy | 241 | AAGAAACTGGGGAGTCTTGAGGAGCCCCCGACTCTCAAGCGGAAACCCCGGATGTGA | 300 | | | | | | |
| Db | 241 | AAGAAACTGGGGAGTCTTGAGGAGCCCCCGACTCTCAAGCGGAAACCCCGGATGTGA | 300 | | | | | | |
| Qy | 301 | GGAGCGGCAATGTGCAATACCAATGCTGTACTCTACTGATGGTGGTGTAAACACCT | 360 | | | | | | |
| Db | 301 | GGAGCGGCAATGTGCAATACCAATGCTGTACTCTACTGATGGTGGTGTAAACACCT | 360 | | | | | | |
| Qy | 361 | CACAGATTCCAGCTTCGGAACAAGACACCCTGGTTAGACCAAGCCATTGCTTTGAAGT | 420 | | | | | | |
| Db | 361 | CACAGATTCCAGCTTCGGAACAAGACACCCTGGTTAGACCAAGCCATTGCTTTGAAGT | 420 | | | | | | |
| Qy | 421 | TATTAAAGTCTGTGGTGCACAAAAGACACTTATGATGAGAAGCAACAATATTGTATATT | 480 | | | | | | |
| Db | 421 | TATTAAAGTCTGTGGTGCACAAAAGACACTTATGATGAGAAGCAACAATATTGTATATT | 480 | | | | | | |
| Qy | 481 | TTGGCCAGTATATTGACTAAACGATTATGATGAGAAGCAACAATATTGTATATT | 540 | | | | | | |
| Db | 481 | TTGGCCAGTATATTGACTAAACGATTATGATGAGAAGCAACAATATTGTATATT | 540 | | | | | | |
| Qy | 541 | GTTCAAATGATCTCTAGAGATTGTTTGGCGTGCAGAGCTTCTCTGTGAAGAGCAACA | 600 | | | | | | |
| Db | 541 | GTTCAAATGATCTCTAGAGATTGTTTGGCGTGCAGAGCTTCTCTGTGAAGAGCAACA | 600 | | | | | | |
| Qy | 601 | GAAAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG | 660 | | | | | | |
| Db | 601 | GAAAAATATATACCATGATCTACAGGAACCTTGGTAGTAGTCAATCAGCAGGAATCATCGG | 660 | | | | | | |
| Qy | 661 | ACTCAGGTACATCTGTGAGTGAACAAGTGTACCTTGAAGTGGGAGTGATCAAAAGG | 720 | | | | | | |
| Db | 661 | ACTCAGGTACATCTGTGAGTGAACAAGTGTACCTTGAAGTGGGAGTGATCAAAAGG | 720 | | | | | | |
| Qy | 721 | ACCTTGACAAAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTTAGACCAT | 780 | | | | | | |
| Db | 721 | ACCTTGACAAAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTTCTTAGACCAT | 780 | | | | | | |

| | | | |
|----|------|---|------|
| Qy | 781 | CTACCTCATCTAGAAGSAGAGCAATTAGTGAGACAGAGAAAATTACAGATGAATATATCTG | 840 |
| Db | 781 | | |
| Qy | 841 | GTGAACGACAAAGAAAAGCCACAAATCTGATAGTATTTCCCTTTCCCTTTGATGAAAGCC | 900 |
| Db | 841 | | |
| Qy | 901 | TGGCTCTGTGTAAATAAGGAGACATAGTTGTGAAGAAGCAGTACGAGTGAATCTACAG | 960 |
| Db | 901 | TGGCTCTGTGTAAATAAGGAGACATAGTTGTGAAGAAGCAGTACGAGTGAATCTACAG | 960 |
| Qy | 961 | GGACGCCATCGAATCCGGATCTTGATGCTGGTGTAAAGTGAACATTCAGGTGATGGTTGG | 1020 |
| Db | 961 | GGACGCCATCGAATCCGGATCTTGATGCTGGTGTAAAGTGAACATTCAGGTGATGGTTGG | 1020 |
| Qy | 1021 | ATCAGGATTCAGTTTCAGATCAGTTTACGTGTAGAAATTTGAAGTTGAATCTCTCCGACTCAG | 1080 |
| Db | 1021 | | |
| Qy | 1081 | AAGATTATAGCCTTAGTGAAGAGACAAAGCAACTCTCAGATGAAGATGATGAGGTATATC | 1140 |
| Db | 1081 | AAGATTATAGCCTTAGTGAAGAGACAAAGCAACTCTCAGATGAAGATGATGAGGTATATC | 1140 |
| Qy | 1141 | AAGTTACTGTCTATCAGCGCAGGGAGAGTGATACAGATTCATTTGAAGAAGATCTCTGAAA | 1200 |
| Db | 1141 | AAGTTACTGTCTATCAGCGCAGGGAGAGTGATACAGATTCATTTGAAGAAGATCTCTGAAA | 1200 |
| Qy | 1201 | TTTCCTTAGCTGACTATTTGGAATGCACTTCATGCAATGAATATGAAATCCCTCTCCAT | 1260 |
| Db | 1201 | TTTCCTTAGCTGACTATTTGGAATGCACTTCATGCAATGAATATGAAATCCCTCTCCAT | 1260 |
| Qy | 1261 | CACATTGCAACAGATGTTGGGCCCTTTCGTGAGAAATTGGCTTTCCTGAAGATAAAGGGAAAG | 1320 |
| Db | 1261 | CACATTGCAACAGATGTTGGGCCCTTTCGTGAGAAATTGGCTTTCCTGAAGATAAAGGGAAAG | 1320 |
| Qy | 1321 | ATAAAGGGAAATCTCTGAGAAAGCCAACTGGAARAACTCAACACAAAGCTGAAGAGGGCT | 1380 |
| Db | 1321 | ATAAAGGGAAATCTCTGAGAAAGCCAACTGGAARAACTCAACACAAAGCTGAAGAGGGCT | 1380 |
| Qy | 1381 | TTGATGTTCTCTGATTGTAAAAAACTATAGTGAATGATCCAGAGAGTCAATGTTGAGG | 1440 |
| Db | 1381 | TTGATGTTCTCTGATTGTAAAAAACTATAGTGAATGATCCAGAGAGTCAATGTTGAGG | 1440 |
| Qy | 1441 | AAAATGATGATAAAATTTACAAAGCTTCACAATCACAAAGAAAGTGAAGACTATTTCTCAGC | 1500 |
| Db | 1441 | AAAATGATGATAAAATTTACAAAGCTTCACAATCACAAAGAAAGTGAAGACTATTTCTCAGC | 1500 |
| Qy | 1501 | CATCAACTCTTAGTAGCATTTATTTATAGCCCAAGAAAGATGTGAAGAAGTTTGAAGGG | 1560 |
| Db | 1501 | CATCAACTCTTAGTAGCATTTATTTATAGCCCAAGAAAGATGTGAAGAAGTTTGAAGGG | 1560 |
| Qy | 1561 | AAGAAACCAAGACAAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTGAAC | 1620 |
| Db | 1561 | AAGAAACCAAGACAAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTGAAC | 1620 |
| Qy | 1621 | CTTGTGTGATTTGTCAAGGTCGACCTTAAAAATGGTTGCATTTGCCATGCCAAAACAGGAC | 1680 |
| Db | 1621 | CTTGTGTGATTTGTCAAGGTCGACCTTAAAAATGGTTGCATTTGCCATGCCAAAACAGGAC | 1680 |
| Qy | 1681 | ATCTTAGGCTCGCTTTACATGTGCAAAAGAGCTAAAGAAGAAAGTAAGSCCTGCCCGAG | 1740 |
| Db | 1681 | ATCTTAGGCTCGCTTTACATGTGCAAAAGAGCTAAAGAAGAAAGTAAGSCCTGCCCGAG | 1740 |
| Qy | 1741 | TATGTAGACACCCAAATTCNAATGATTTGCTTAACCTATTTTCCCTTAGTTGACCTGCTCAT | 1800 |
| Db | 1741 | TATGTAGACACCCAAATTCNAATGATTTGCTTAACCTATTTTCCCTTAGTTGACCTGCTCAT | 1800 |
| Qy | 1801 | AAGAGAAATATATATTTCTTAACCTATATAACCCCTAGGAATTTAGACAACCTGAAATTTAT | 1860 |
| Db | 1801 | AAGAGAAATATATATTTCTTAACCTATATAACCCCTAGGAATTTAGACAACCTGAAATTTAT | 1860 |

RESULT 13

RESULT 13
US-09-280-805-1

US-09-280-805-1 : Sequence 1 Application US/09280805

```

; Sequence 1, Application
; Date: 6/19/2012

```

; Patent No. 6184212
; CENTRAL INFORMATION.

; GENERAL INFORMATION:

APPLICANT: Loren J. Miraglia, Pam

; APPLICANT: Graham, Brett P. Monia

; TITLE OF INVENTION: ANTISENSE IN

1. TITLE OF INVENTION: EXPERIMENTAL

NUMBER OF SEQUENCES: 2

NUMBER OF SEQUENCES: 471
CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS: ADDRESSEE: Law Offices of J

STREET: 66 Ea

STREET: 66 Ea
CITY: Marlton

CITY: Marlton
STATE: NJ

STATE: NJ

; COUNTRY: U.S.A.

ZIP: 08053

; COMPUTER READABLE F

MEDIUM TYPE: DISKETTE, 3.5 I

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;
;
COMPUTER: IBM PC
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COMPUTER: IBM FC
OPERATING SYSTEM: WIND

OPERATING SYSTEM: WINDOWS 3.11
SOFTWARE: WORDPERFECT 6.0

```

; SOFTWARE: WORDPERFECT
; CURRENT APPLICATION DATA:

```

APPLICANT'S NAME _____
ADDRESS _____
CITY _____ STATE _____ ZIP _____
TELEPHONE _____

DATE OF BIRTH _____ SEX _____
MARRIAGE DATE _____
CHILDREN _____
EDUCATION _____
OCCUPATION _____
REASON FOR APPLICATING _____
REFERENCES _____
SIGNATURE _____
DATE _____

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; APPLICATION NUMBER:
; FILING DATE:
;

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; FILING DATE: herewith

; CLASSIFICATION:

;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/048,

FILING DATE: March 26, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Licata, Jane Massey

NAME: LUCICA, JAMIE MASSEY
REGISTRATION NUMBER: 32,257

REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2372 base pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Unknown

; ANTI-SENSE: NO

; PUBLICATION INFORMATION:

; AUTHORS: Oliner, J. D.

; AUTHORS: Kinzler, K. W.

; AUTHORS: Meltzer, P. S.

; AUTHORS: George, D. L.

; AUTHORS: Vogelstein, B.

; TITLE: Amplification of a gene encoding a

; TITLE: p53-associated protein in human sarcomas

; JOURNAL: Nature

; VOLUME: 358

; ISSUE: 6381

; PAGES: 80-83

; DATE: 02-JUL-1992

; US-09-280-805-1

Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACCGCGGAGCTGGCTCTTCTGGGGCTGTGTGGCCCTGTGTGTCGGAAGATGGA 60
DB 1 GCACCGCGGAGCTGGCTCTTCTGGGGCTGTGTGGCCCTGTGTGTCGGAAGATGGA 60

QY 61 GCAGAGCCGAGCCGAGGGGGCGGACCCCTCTGACCGAGATCCTGCTGTTTCG 120
DB 61 GCAGAGCCGAGCCGAGGGGGCGGACCCCTCTGACCGAGATCCTGCTGTTTCG 120

QY 121 CAGCCAGGAGCAGCCGCTCCCTCCCGGATAGTGCCTACAGCGCCGAGTGCCTGGCCG 180
DB 121 CAGCCAGGAGCAGCCGCTCCCTCCCGGATAGTGCCTACAGCGCCGAGTGCCTGGCCG 180

QY 181 GAGAGTGAATGATCCCGAGGCGGAGGGCTGCTGCTTCCCGAGTAGTGCAGTCCCGCG 240
DB 181 GAGAGTGAATGATCCCGAGGCGGAGGGCTGCTGCTTCCCGAGTAGTGCAGTCCCGCG 240

QY 241 AAGAAATCGGGAGTCTTGAGGAGCCCCGACTCCAAAGCGGAAACCCCGATGTTGA 300
DB 241 AAGAAATCGGGAGTCTTGAGGAGCCCCGACTCCAAAGCGGAAACCCCGATGTTGA 300

QY 301 GGAGCGCAAAATGTCGAATACCAACATGCTCTGCTACTACTGATGGTGTGTAACCACT 360
DB 301 GGAGCGCAAAATGTCGAATACCAACATGCTCTGCTACTACTGATGGTGTGTAACCACT 360

QY 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATGCTTTTGAAGT 420
DB 361 CACAGATTCAGCTTCGGAACAAGAGACCCCTGGTTAGACCAAGCCATGCTTTTGAAGT 420

QY 421 TATTAAAGTCTGTTGGTGCACAAAGACACATTAATGATGAGAGGTTCTTTTATC 480
DB 421 TATTAAAGTCTGTTGGTGCACAAAGACACATTAATGATGAGAGGTTCTTTTATC 480

QY 481 TTGGCCAGTATATGACTAAACGATTAATGATGAGAGCAACAAACATATTGTAAT 540
DB 481 TTGGCCAGTATATGACTAAACGATTAATGATGAGAGCAACAAACATATTGTAAT 540

QY 541 GTTCAATGATCTTCTAGGAGATTTGTTGGCGTGCACAGCTTCTCTGTGGAAGAGACA 600
DB 541 GTTCAATGATCTTCTAGGAGATTTGTTGGCGTGCACAGCTTCTCTGTGGAAGAGACA 600

QY 601 GGAAATATATACCATGATCTACAGGAACCTGGTAGTGTAGTCAATCAGCAGGAATCATCG 660
DB 601 GGAAATATATACCATGATCTACAGGAACCTGGTAGTGTAGTCAATCAGCAGGAATCATCG 660

QY 661 ACTCAGGTACATCTGTCAGTGAGAACAGGTGTCACCTTGAAGGTGGGAGTGTATCAAAAG 720
DB 661 ACTCAGGTACATCTGTCAGTGAGAACAGGTGTCACCTTGAAGGTGGGAGTGTATCAAAAG 720

QY 721 ACCTGTACAAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTCTAGACCAT 780
DB 721 ACCTGTACAAGAGCTTCAGGAAGAGAAACCTTCATCTTCACATTTGGTTCTAGACCAT 780

QY 781 CTACCTCATCTAGAAGGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATATCTG 840
DB 781 CTACCTCATCTAGAAGGAGCAATTTAGTGAGACAGAGAAATTCAGATGAATATCTG 840

QY 841 GTGAACGACAAAGAAACCCACAAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC 900
DB 841 GTGAACGACAAAGAAACCCACAAATCTGATAGTATTTCCCTTTCTTTGATGAAGCC 900

QY 901 TGGCTCTGTGTGTAATAGGGAGATATTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960
DB 901 TGGCTCTGTGTGTAATAGGGAGATATTTGTGAAGAGCAGTAGCAGTGAATCTACAG 960

QY 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATGTTGG 1020
DB 961 GGACGCCATCGAATCCGGATCTTGATGCTGGTGAAGTGAACATTCAGGTGATGTTGG 1020

QY 1021 ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGAAATTTGAAGTGAATCTCGACTCAG 1080
DB 1021 ATCAGGATTCAGTTTCAGATCAGTTTAGTGTAGAAATTTGAAGTGAATCTCGACTCAG 1080

QY 1081 AAGATTATAGCCTTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGAGGTATATC 1140
DB 1081 AAGATTATAGCCTTAGTGAAGAGCAAGAACTCTCAGATGAAGATGATGAGGTATATC 1140

QY 1141 AAGTTACTGTGTATCAGCAGGGGAGAGTATACAGATTCATTTGAAGAGATTCCTGAAA 1200
DB 1141 AAGTTACTGTGTATCAGCAGGGGAGAGTATACAGATTCATTTGAAGAGATTCCTGAAA 1200

QY 1201 TTTCTTACGTGACTATTTGGAAATGCACTTCATCAATGAATGAATCCCCCTTCCAT 1260
DB 1201 TTTCTTACGTGACTATTTGGAAATGCACTTCATCAATGAATGAATCCCCCTTCCAT 1260

QY 1261 CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCTGAGATTAAGGNAAG 1320
DB 1261 CACATTGCAACAGATGTTGGGCCCTTCGTGAGAAATTTGGCTTCTGAGATTAAGGNAAG 1320

QY 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAGCTGAAGGGCT 1380
DB 1321 ATAAAGGGGAAATCTCTGAGAAAGCCAAACTGGAATACTCAACACAGCTGAAGGGCT 1380

QY 1381 TTGATGTTCTCTGATTTAAAAAACTATAGTAATGATTTCCAGAGATCATGTTGAGG 1440
DB 1381 TTGATGTTCTCTGATTTAAAAAACTATAGTAATGATTTCCAGAGATCATGTTGAGG 1440

QY 1441 AAAATGATGATAAAATTTACAAAGCTTCACAAATCACAAGAAAGTGAAGACTATTCACAG 1500
DB 1441 AAAATGATGATAAAATTTACAAAGCTTCACAAATCACAAGAAAGTGAAGACTATTCACAG 1500

QY 1501 CATCAACTTCTAGTAGCATTTATAGCAGCCAGAGATGTTGAAGAGTTTGAAGGG 1560
DB 1501 CATCAACTTCTAGTAGCATTTATAGCAGCCAGAGATGTTGAAGAGTTTGAAGGG 1560

QY 1561 AAGAAACCCCAAGACAAAGAGAGTGTGGAATCTAGTTTCCCTTAATGTCATTGAAC 1620
DB 1561 AAGAAACCCCAAGACAAAGAGAGTGTGGAATCTAGTTTCCCTTAATGTCATTGAAC 1620

QY 1621 CTTGTGTGATTTGTCAGAGTGCAGCTTAAATGTTGCTGATTTCCATGGCAAAACAGGAC 1680
DB 1621 CTTGTGTGATTTGTCAGAGTGCAGCTTAAATGTTGCTGATTTCCATGGCAAAACAGGAC 1680

QY 1681 ATCTTATGSCCTGCTTTACATGTCGAAAGAGCTTAAAGAAAGAAATTAAGCCCTGCCAG 1740
DB 1681 ATCTTATGSCCTGCTTTACATGTCGAAAGAGCTTAAAGAAAGAAATTAAGCCCTGCCAG 1740

QY 1741 TATGTAGACAACCAATTTCAATGATTTGCTAACTTATTTCCCTTAGTTCACCTGCTAT 1800
DB 1741 TATGTAGACAACCAATTTCAATGATTTGCTAACTTATTTCCCTTAGTTCACCTGCTAT 1800

QY 1801 AAGAGAAATATATATTTCTTAACATATATATACCCCTAGGAATTTAGACAACCTGAATTTATT 1860
Db 1801 AAGAGAAATATATATTTCTTAACATATATATACCCCTAGGAATTTAGACAACCTGAATTTATT 1860
QY 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTTACATAGATTTCTTCTTTAGTATAAT 1920
Db 1861 CACATATATCAAAAGTGAAGAAATGCTCAATTTACATAGATTTCTTCTTTAGTATAAT 1920
QY 1921 TGACCTACTTTGGTACTGGAATAGTAATACCTTACTATAATTTGACTTGAATATGAGCT 1980
Db 1921 TGACCTACTTTGGTACTGGAATAGTAATACCTTACTATAATTTGACTTGAATATGAGCT 1980
QY 1981 CATCTCTTACACCAACTCTTAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
Db 1981 CATCTCTTACACCAACTCTTAATTTAAATAATTTCTACTCTGTCTTAAATGAGAAGTAC 2040
QY 2041 TTGGTTTTTTTTTCTTAATATGATATGACATTTAAATGAACTTAAATTTATTTTGTG 2100
Db 2041 TTGGTTTTTTTTTCTTAATATGATATGACATTTAAATGAACTTAAATTTATTTTGTG 2100
QY 2101 AGACCGAGTCTTCTGTTTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
Db 2101 AGACCGAGTCTTCTGTTTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
QY 2161 AGCTCTGCCCTCCCGGGTTCGACCACTTCTCTGCTCAGCTCCCAATGAGCTTGCC 2220
Db 2161 AGCTCTGCCCTCCCGGGTTCGACCACTTCTCTGCTCAGCTCCCAATGAGCTTGCC 2220
QY 2221 TACAGTCACTGCGCACCACTGCGTAAATTTTGTACTTTTGTAGAGACAGGTTTC 2280
Db 2221 TACAGTCACTGCGCACCACTGCGTAAATTTTGTACTTTTGTAGAGACAGGTTTC 2280
QY 2281 ACCGTGTTAGCCAGGATGCTGATCTCTGACCTCTGATCCCGCCACCTCGGCTCC 2340
Db 2281 ACCGTGTTAGCCAGGATGCTGATCTCTGACCTCTGATCCCGCCACCTCGGCTCC 2340
QY 2341 CAAAGTCTGGGATACAGCATGAGCCACG 2372
Db 2341 CAAAGTCTGGGATACAGCATGAGCCACG 2372

RESULT 14

US-09-048-810-1
; Sequence 1, Application US/09048810
; Patent No. 6238921
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: MODULATION OF HUMAN MD2 EXPRESSION
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,810
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0302
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-779-2400

TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: No
; PUBLICATION INFORMATION:
; AUTHORS: Oliner, J.D.
; AUTHORS: Kinzler, K.W.
; AUTHORS: Meltzer, P.S.
; AUTHORS: George, D.L.
; AUTHORS: Vogelstein, B.
; TITLE: Amplification of a gene encoding a
; TITLE: p53-associated protein in human sarcomas
; JOURNAL: Nature
; VOLUME: 358
; ISSUE: 6381
; PAGES: 80-83
; DATE: 02-JUL-1992
; US-09-048-810-1
Query Match 100.0%; Score 2372; DB 4; Length 2372;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCACCCGGCAGCTTGGCTGCTTCTGGGGCCCTGCTGGCCCTGCTGTCGGAAGATGGA 60
Db 1 GCACCCGGCAGCTTGGCTGCTTCTGGGGCCCTGCTGGCCCTGCTGTCGGAAGATGGA 60
QY 61 GCAAGAACGCGAGCCGCGAGGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTCG 120
Db 61 GCAAGAACGCGAGCCGCGAGGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTCG 120
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 Qy 1741 TAGTACAGAACCAATTCATGCTGCTACTTATTTCCCTAGTTGACCTGCTAT 1800
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 Db 2221 TACAGTCACTGCGCCACACACCTGGCTAATTTTGTGACTTTTAGTAGACAGAGGTTTC 2280
 Qy 2281 ACCGTGTAGCCAGAGTGTCTCGATCTCTGATCTCTGATCCGCTCGGCTCGGCTCC 2340
 Db 2281 ACCGTGTAGCCAGAGTGTCTCGATCTCTGATCTCTGATCCGCTCGGCTCGGCTCC 2340
 Qy 2341 CAAAGTGTGGGATTCAGGATGAGCCACCG 2372
 Db 2341 CAAAGTGTGGGATTCAGGATGAGCCACCG 2372

RESULT 15
 US-09-170-159A-2
 ; Sequence 2, Application US/09170159A
 ; Patent No. 6399755
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; HILL, DAVID E.
 ; KINZLER, KENNETH W.
 ; VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 13-Oct-1998
 ; CLASSIFICATION: <unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAGAN, SARAH A.
 ; REGISTRATION NUMBER: 32,141

| | | | | |
|----|------|--|--|------|
| Db | 1741 | | TATGTAGACAACCAATTCAAATGATGTGCTAACTTATTTCCCTAGTTGACCTGCTCTAT | 1800 |
| Qy | 1801 | | AAGAGAAATTATATATTTCTAACTATATTAACCTAGGAATTTAGACAACCTGAAATTTAT | 1860 |
| Db | 1801 | | AAGAGAAATTATATATTTCTAACTATATTAACCTAGGAATTTAGACAACCTGAAATTTAT | 1860 |
| Qy | 1861 | | CACATATATCAAAAGTGAGAAAATGCGTCAATTCACATAGATTTCTCTCTTTAGTATAAT | 1920 |
| Db | 1861 | | CACATATATCAAAAGTGAGAAAATGCGTCAATTCACATAGATTTCTCTCTTTAGTATAAT | 1920 |
| Qy | 1921 | | TGACCTACTTTGGTACTGAGTGAATGACTTACTATTAATTTGACTTGAATATGTAGCT | 1980 |
| Db | 1921 | | TGACCTACTTTGGTACTGAGTGAATGACTTACTATTAATTTGACTTGAATATGTAGCT | 1980 |
| Qy | 1981 | | CATCCTTTTACACCAACTCCTAAATTTTAAATTTTCTACTCTGTCTTAAATGAGAAGTAC | 2040 |
| Db | 1981 | | CATCCTTTTACACCAACTCCTAAATTTTAAATTTTCTACTCTGTCTTAAATGAGAAGTAC | 2040 |
| Qy | 2041 | | TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTTTTTG | 2100 |
| Db | 2041 | | TTGGTTTTTTTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTTTTTG | 2100 |
| Qy | 2101 | | AGACCGAGTCTTCTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA | 2160 |
| Db | 2101 | | AGACCGAGTCTTCTCTGTGTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA | 2160 |
| Qy | 2161 | | AGCTCTGCCCTCCCGGGTTCCGACCAATTTCTCTGCTCAGCCTCCCAATTAGCTTGGCC | 2220 |
| Db | 2161 | | AGCTCTGCCCTCCCGGGTTCCGACCAATTTCTCTGCTCAGCCTCCCAATTAGCTTGGCC | 2220 |
| Qy | 2221 | | TACAGTCATCTGCCACCACTGGCTAATTTTGTACTTTTGTAGTAGACAGGGTTTC | 2280 |
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| Qy | 2281 | | ACCGTGTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC | 2340 |
| Db | 2281 | | ACCGTGTAGCCAGGATGCTCGATCTCCTGACCTCGTGATCCGCCACCTCGGCCCTCC | 2340 |
| Qy | 2341 | | CAAAAGTCTGGGATTTACAGGCATGAGCCACCG | 2372 |
| Db | 2341 | | CAAAAGTCTGGGATTTACAGGCATGAGCCACCG | 2372 |

Search completed: January 9, 2003, 13:40:56
Job time : 91 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2003, 10:51:14 ; Search time 3329 Seconds
(without alignments)
11539.710 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcaacgcgcagcttgctg.....attacagcgatgagccacg 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16134066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: em_esthum:*
3: em_estlin:*
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7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
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20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 1001 | 42.2 | 3028 | 11 AK004719 | AK004719 Mus muscu |
| 2 | 701.2 | 29.6 | 743 | 9 AI927905 | AI927905 wp03c08.x |
| 3 | 679.4 | 28.6 | 709 | 12 BF057574 | BF057574 7x46c07.x |
| 4 | 658.8 | 27.8 | 970 | 13 BM479400 | BM479400 AGENCOURT |
| 5 | 633.4 | 26.7 | 3007 | 11 AK004881 | AK004881 Mus muscu |
| 6 | 612 | 25.8 | 778 | 12 BE900427 | BE900427 601673652 |

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| 13 | 526.4 | 22.2 | 537 | 17 AQ077720 | AQ077720 CIT-HSP-2 |
| 14 | 519 | 21.9 | 555 | 10 BE296905 | BE296905 601176992 |
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| 16 | 474.2 | 20.0 | 578 | 12 BF043301 | BF043301 nab37q05 |
| 17 | 463.4 | 19.5 | 523 | 12 BF045166 | BF045166 BP250026B |
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| 19 | 449.4 | 18.9 | 476 | 10 BE676440 | BE676440 7f29h02.x |
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| 23 | 418.8 | 17.7 | 696 | 13 BI150617 | BI150617 602914985 |
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| 27 | 402.6 | 17.0 | 427 | 9 AA214617 | AA214617 zt88h09.s |
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| 30 | 389.8 | 16.4 | 617 | 10 AW822859 | AW822859 ug21a07.y |
| 31 | 386.8 | 16.3 | 579 | 12 BG081785 | BG081785 H3069A07- |
| 32 | 381.2 | 16.1 | 583 | 13 BM055838 | BM055838 i083f05.y |
| 33 | 377 | 15.9 | 377 | 12 BF155177 | BF155177 OVO-BT084 |
| 34 | 376.2 | 15.9 | 647 | 12 BG080240 | BG080240 H3051D04- |
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| 37 | 345.8 | 14.6 | 580 | 10 BE308548 | BE308548 601102803 |
| 38 | 341 | 14.4 | 556 | 12 BF548539 | BF548539 UI-R-AO-a |
| 39 | 338.2 | 14.3 | 486 | 10 AW070956 | AW070956 xa31h03.x |
| 40 | 331 | 14.0 | 393 | 9 AL704062 | AL704062 DKF2p686N |
| 41 | 327.4 | 13.8 | 345 | 12 BE765314 | BE765314 IL2-NT010 |
| 42 | 327 | 13.8 | 738 | 13 BG977125 | BG977125 602846256 |
| 43 | 320.2 | 13.5 | 366 | 9 AA568852 | AA568852 nm27a12.s |
| 44 | 315.6 | 13.3 | 611 | 13 BI296301 | BI296301 UI-R-DK0- |
| 45 | 315 | 13.3 | 674 | 12 BF161075 | BF161075 601786015 |

ALIGNMENTS

RESULT 1

AK004719

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

AK004719 3028 bp mRNA linear HTC 19-JAN-2002
Mus musculus adult male lung CDNA, RIKEN full-length enriched
library, clone:1200011P22;transformed mouse 3T3 cell double minute
2, full insert sequence.

AK004719 1 GI:12836100
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) adult male lung CDNA to mRNA,
clone_lib:RIKEN full-length enriched mouse CDNA library
clone:1200011P22.

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length CDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

20499374
20499374
11042159


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similar to SW:MDM2_HUMAN Q00987 MDM2 PROTEIN ; mRNA sequence.
ACCESSION
BF057574
VERSION
BF057574.1 GI:10811470
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 709)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento
Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 481.
FEATURES
source
1..709
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/db_xref="taxon:9606"
/clone="IMAGE:347825"
/clone_lib="NCI-CGAP-Ov18"
/tissue_type="fibrothoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: ovary; Vector: p773D-Pac (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCGACATTTTCTTTTCTTTT 3'];
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

```
BASE COUNT 197 a 163 c 175 g 172 t 2 others
ORIGIN
Query Match 28.6%; Score 679.4; DB 12; Length 709;
Best Local Similarity 97.9%; Pred. No. 4.9e-119;
Matches 700; Conservative 0; Mismatches 8; Indels 7; Gaps 1;
QY 100 ACCGAGATCCCTGCTGCTTTCGACGCCAGGAGCACCCTCCCTCCCGGATTAGTGGGTAGC 159
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QY 220 CGCGAGTAGTACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279
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QY 580 GCTTCTCTGTAAGACAGACAGGAAATATATACCATGATCTCAGGAACTTGGTAGTAG 639
Db 474 GCTTCTCTGTAAGACAGACAGGAAATATATACCATGATCTCAGGAACTTGGTAGTAG 533
QY 640 TCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGACAGGTGTCACCTTG 699
Db 534 TCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGACAGGTGTCACCTTG 593
QY 700 AAGGTGGAGTTCATCAAAAGGACCTTGTACAGAGCTTTCAGGAGAGAAACCTTCACTT 759
Db 594 AAGGTGGAGTTCATCAAAAGGACCTTGTACAGAGCTTTCAGGAGAGAAACCTTCACTT 653
QY 760 CACATTTGTTTCTAGACCACTCTACCTCATCTAGAACGAGCAATTAGTGAGAC 814
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| Db | 654 | CACATTTGGTTCTAGACCATCTACCTCATCTAGAAAGAGACAAATTTGTGAGAC | 708 |
|-----------------------|--------------|--|---------------|
| RESULT 4 | | | |
| BM479400 | | | |
| LOCUS | | | |
| DEFINITION | | | |
| ACCESSION | | | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| COMMENT | | | |
| FEATURES | | | |
| Source | | | |
| BASE COUNT | 290 | 186 | 232 |
| ORIGIN | | | |
| Query Match | 27.88 | Score 658.8 | DB 13 |
| Best Local Similarity | 97.48 | Prod. 3.7e-115 | Length 970 |
| Matches 699 | Conservative | 0 | Mismatches 16 |
| | | | Indels 3 |
| | | | Gaps 3 |
| QY | 305 | CAGGCAATGTGCAATACCAACATGTCTGTACCTACTGATGTGTGTGACACCCATTCCTTTTCAAGTTATT | 364 |
| Db | 69 | CAGGCAATGTGCAATACCAACATGTCTGTACCTACTGATGTGTGTGACACCCATTCCTTTTCAAGTTATT | 128 |
| QY | 365 | GATTCACGCTTCGGAAACAAGAGACCCCTGGTTAGACAAAGCCATTCCTTTTCAAGTTATT | 424 |
| Db | 129 | GATTCACGCTTCGGAAACAAGAGACCCCTGGTTAGACAAAGCCATTCCTTTTCAAGTTATT | 188 |
| QY | 425 | AAAGTCTGTGTGCAACAAAGACACTTATCTATGAAAGAGGTTCTTTTTTATCTTGG | 484 |
| Db | 189 | AAAGTCTGTGTGTCACAAAAGACACTTATCTATGAAAGAGGTTCTTTTTTATCTTGG | 248 |
| QY | 485 | CCAGTATATTATGACTAAACGATTATATGATGAGAAGCAACACATATTGTATTGTTC | 544 |
| Db | 249 | CCAGTATATTATGACTAAACGATTATATGATGAGAAGCAACACATATTGTATTGTTC | 308 |
| QY | 545 | AAATGATCTCTAGAGATTCTTTTGGCGTCCCAAGCTTCTCTGTCAAAGACACAGAA | 604 |
| Db | 309 | AAATGATCTCTAGAGATTCTTTTGGCGTCCCAAGCTTCTCTGTCAAAGACACAGAA | 368 |
| QY | 605 | AAATATACCATGATCTACAGAACTTTGGTAGTAGTCAATACGACGAGAAATATCGACTC | 664 |
| Db | 369 | AAATATACCATGATCTACAGAACTTTGGTAGTAGTCAATACGACGAGAAATATCGACTC | 428 |

Email: cgapbs-re@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/Image/Image.html
 Seq primer: M13 Forward.

FEATURES
 source
 1. .612
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3077314"
 /clone_lib="NIH_MGC_50"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
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 /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (3.5-4.4kb). Directionally cloned. Cells provided by
 Louis M. Staudt, Ph.D. Library preparation by Maria de
 Fatima B. Staudt, Ph.D. and M. Bento Soares, Ph.D."
 BASE COUNT 197 a 103 c 149 g 163 t

Query Match 25.6%; Score 606.4; DB 10; Length 612;
 Best Local Similarity 99.8%; Pred. No. 3.6e-105;
 Matches 607; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 511 ATGATGAGAGCAACACATATTGTATATTTGTTCAATGATCTCTAGGAGATTGTTG 570
 DB 5 AGGATGAGAGCAACACATATTGTATTTGTTCAATGATCTCTAGGAGATTGTTG 64
 QY 571 GCGTGCCAGCTTCTCTGTTGAAGAGCAGAGAAATATATACATGATCTACAGAACT 630
 DB 65 GCGTGCCAGCTTCTCTGTTGAAGAGCAGAGAAATATATACATGATCTACAGAACT 124
 QY 631 TGGTAGTAGTCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGAACAGGT 690
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 QY 691 GTCACTTGAGCTGGAGTATCAAGAGGACCTGTACAGAGCTTCAGAGAGAAAC 750
 DB 185 GTCACTTGAGCTGGAGTATCAAGAGGACCTGTACAGAGCTTCAGAGAGAAAC 244
 QY 751 CTTCACTTCCACATTTGGTTCTAGACCATCTACCTCATCTAGAGGAGCAATTAGTG 810
 DB 245 CTTCACTTCCACATTTGGTTCTAGACCATCTACCTCATCTAGAGGAGCAATTAGTG 304
 QY 811 AGACAGAGAAATTCAGATGAATATCTGTTGAAGCAAGAAACGCCACAAATCTG 870
 DB 305 AGACAGAGAAATTCAGATGAATATCTGTTGAAGCAAGAAACGCCACAAATCTG 364
 QY 871 ATAGATTTCCCTTCCCTTTGATGAAGCCTGGCTCTGTGTGTAATAGGAGATATGTT 930
 DB 365 ATAGATTTCCCTTCCCTTTGATGAAGCCTGGCTCTGTGTGTAATAGGAGATATGTT 424
 QY 931 GTGAAGAACAGCTAGCAGTGAATCTACAGGAGCCCATCGAATCCGGATCTTGATGCTG 990
 DB 425 GTGAAGAACAGCTAGCAGTGAATCTACAGGAGCCCATCGAATCCGGATCTTGATGCTG 484
 QY 991 GTGTAGTGAACTTACAGTGATTTGGTGGATCAGGATTCAGATCAGTTTAGTG 1050
 DB 485 GTGTAGTGAACTTACAGTGATTTGGTGGATCAGGATTCAGATCAGTTTAGTG 544
 QY 1051 TAGAATTTGAAGTTGAATCTCTCGACTCAGAGATTTATAGCCTTAGTCAAGAGCAAG 1110
 DB 545 TAGAATTTGAAGTTGAATCTCTCGACTCAGAGATTTATAGCCTTAGTCAAGAGCAAG 604
 QY 1111 AACTCTCA 1118

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 Db 605 AACTCTCA 612

RESULT 8
 BI335419/c
 LOCUS
 DEFINITION
 BI335419
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 773)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-re@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM1346 row: e column: 01
 High quality sequence stop: 771.
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:5140584"
 /clone_lib="NIH_MGC_12"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: pCMV-SpORF6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 BASE COUNT 212 a 157 c 139 g 265 t

ORIGIN
 Query Match 25.4%; Score 603; DB 13; Length 773;
 Best Local Similarity 99.0%; Pred. No. 1.5e-104;
 Matches 617; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1200 ATTTCTCTAGCTGACATTTGGAATGCATTCATGCAATGAATGAATCCCCCTTCCA 1259
 DB 622 ATTTCTTTGAAGGACATTTGGAATGCATTCATGCAATGAATGAATCCCCCTTCCA 563
 QY 1260 TCACATTCACACAGATTTGGGCGCTTCGTGAGATTCGCTTCCTGAAGATAAGGAAA 1319
 DB 562 TCACATTCACACAGATTTGGGCGCTTCGTGAGATTCGCTTCCTGAAGATAAGGAAA 503
 QY 1320 GATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAAAGCTGAAGAGGC 1379
 DB 502 GATAAAGGGGAATCTCTGAGAAAGCCAACTGGAAGAACTCAACACAAAGCTGAAGAGGC 443
 QY 1380 TTTGATCTTCTGATTTAAAAAACTATAGTGAATGATTCAGAGAGTCTATGTTGAG 1439
 DB 442 TTTGATCTTCTGATTTAAAAAACTATAGTGAATGATTCAGAGAGTCTATGTTGAG 383
 QY 1440 GAAATGATGATTAATACAAAGCTTCACAAATCACAAGAAAGTGAAGACTATTCTCAG 1499
 DB 382 GAAATGATGATTAATACAAAGCTTCACAAATCACAAGAAAGTGAAGACTATTCTCAG 323
 QY 1500 CCATCAACTTCTAGTAGCATTTATATAGCAGCCCAAGAGATGTGAAGAGTTTGAAGG 1559
 DB 322 CCATCAACTTCTAGTAGCATTTATATAGCAGCCCAAGAGATGTGAAGAGTTTGAAGG 263


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QY 1560 CAAGAAACCCAGCAAGAGAGAGTGTGGAATAGTGTGGCCCTTAATGCAATGAA 1619
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DB 262 GAAGAAACCCAGCAAGAGAGAGTGTGGAATAGTGTGGCCCTTAATGCAATGAA 203
|||||
QY 1620 CCTTGTGTGATTTGTCAAGGTGACCTAAATAGTGTGCAATGTCATGGCAAGCA 1679
|||||
DB 202 CCTTGTGTGATTTGTCAAGGTGACCTAAATAGTGTGCAATGTCATGGCAAGCA 144
|||||
QY 1680 CATCTTATGCGCTGCTTTACATGTGCAAGAGAGAGTGTGCAATGTCATGGCA 1739
|||||
DB 143 CATCTTATGCGCTGCTTTACATGTGCAAGAGAGAGTGTGCAATGTCATGGCA 84
|||||
QY 1740 GTATGTAGCAACCAATTCATGATGCTAAATAGTGTGCAATGTCATGGCA 1799
|||||
DB 83 GTATGTAGCAACCAATTCATGATGCTAAATAGTGTGCAATGTCATGGCA 24
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QY 1800 TAAGAGAAATATATATTTCTAAC 1822
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DB 23 TAAGAGAAATATATATTTCTAAC 1
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RESULT 9
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LOCUS
DEFINITION
UT-HF-BN0-akj-b-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
IMAGE:3077318 5', mRNA sequence.
ACCESSION
AW500516
VERSION
AW500516.1 GI:7113204
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 571)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3077318"
/clone_lib="NIH_MGC_50"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/lab_host="DH10B (LTI)"
/notes="Vector: p773-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 180 a 96 c 140 g 155 t
ORIGIN
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Query Match 23.8%; Score 565.4; DB 10; Length 571;
Best Local Similarity 99.8%; Pred. No. 2.2e-97;
Matches 566; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 511 ATGATGAGAGCAACATATTTGATTTGTTCAATGATCTTAGGAGATTTGTTG 570
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DB 5 AGGATGAGAGCAACACATATTTGTTTCAATGATCTTCTAGGAGATTTGTTG 64
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QY 571 GCCTGCCAAGCTTCTGTTGAAAAGACACAGGAAAATATATACCATGATCTACAGAACT 630
|||||
DB 65 GCGTGCCAAAGCTTCTGTTGAAAAGACACAGGAAAATATATACCATGATCTACAGAACT 124
|||||
QY 631 TGGTAGTAGTCAATACAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGAACAGGT 690
|||||
DB 125 TGGTAGTAGTCAATACAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGAACAGGT 184
|||||
QY 691 CTCACCTTGAAGGTGGGAGTGATCAAAAGGACCTTCTCAAGAGCTTTCAGGAGAGAAAC 750
|||||
DB 185 CTCACCTTGAAGGTGGGAGTGATCAAAAGGACCTTCTCAAGAGCTTTCAGGAGAGAAAC 244
|||||
QY 751 CTTCACTCTCAATTTGGTTTCTAGACCATCTACCTCATCTAGAGGAGAGCAATAGTG 810
|||||
DB 245 CTTCACTCTCAATTTGGTTTCTAGACCATCTACCTCATCTAGAGGAGAGCAATAGTG 304
|||||
QY 811 AGACAGAGAAATTCAGATGAATTTCTGTTGAACGACCAAAAGAAACCCCAAACTCG 870
|||||
DB 305 AGACAGAGAAATTCAGATGAATTTCTGTTGAACGACCAAAAGAAACCCCAAACTCG 364
|||||
QY 871 ATAGTATTTCCCTTCTGTTGAAAAGCTGCTGTTGTAATTAAGGGAGATATGTT 930
|||||
DB 365 ATAGTATTTCCCTTCTGTTGAAAAGCTGCTGTTGTAATTAAGGGAGATATGTT 424
|||||
QY 931 GTGAAGAGCACTAGCAGTGAATCTACAGGAGCGCCATCGAATCCGATCTTGTATGCTG 990
|||||
DB 425 GTGAAGAGCACTAGCAGTGAATCTACAGGAGCGCCATCGAATCCGATCTTGTATGCTG 484
|||||
QY 991 GTGTAAGTGAACATTCAGGTGATTTGTTGATCAGGATTCAGTTCAGATCAGTTTACTG 1050
|||||
DB 485 GTGTAAGTGAACATTCAGGTGATTTGTTGATCAGGATTCAGTTCAGATCAGTTTACTG 544
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RESULT 10
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LOCUS
DEFINITION
IL4-CT0079-200899-001-B01 CT0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW176629
VERSION
AW176629.1 GI:6442666
KEYWORDS
EST.
SOURCE
human.
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 573)
AUTHORS
HCCP http://www.ludwig.org.br/ORESTES.
TITLE
The FAPESP/LICR Human Cancer Genome Project
JOURNAL
Unpublished (1999)
COMMENT
Contact: Simpson A. J. G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL4&t2=IL4-CT0079-
200899-001-B01&t3=1999-08-20&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 472.
Location/Qualifiers
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1. .573
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/db_xref="taxon:9606"
/clone_lib="CT0079"
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/dev_stage="Adult"
/note="Organ: colon; Vector: pUC18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 184 a 96 c 137 g 155 t 1 others
ORIGIN

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Query Match 23.8% Score 564.6; DB 10; Length 573;
Best Local Similarity 99.1%; Pred. No. 3.1e-97;
Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 518 GAAGCAACAATATGTTGTTCAATATCTCTAGAGATTTGTTGGGTGCC 577
Dbb 1 GAAGCAACAATATGTTGTTCAATATCTCTAGAGATTTGTTGGGTGCC 60
QY 578 AAGCTTCTCTGTAAGAGCAGACAGAAATATATACATGATCTACAGGAATCTGTTAGT 637
Dbb 61 AAGCTTCTCTGTAAGAGCAGACAGAAATATATACATGATCTACAGGAATCTGTTAGT 120
QY 638 AGTCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGACAGGTGTCACCT 697
Dbb 121 AGTCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTGAGACAGGTGTCACCT 180
QY 698 TGAAGTGGGAGTATCAAAAGGACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATC 757
Dbb 181 TGAAGTGGGAGTATCAAAAGGACCTTGTACAGAGCTTCAGGAAGAGAAACCTTCATC 240
QY 758 TTCACATTTGTTTCTAGACCATCTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGA 817
Dbb 241 TTCACATTTGTTTCTAGACCATCTACCTCATCTAGAGGAGAGCAATTTAGTGAGACAGA 300
QY 818 AGAAATTCAGATCAATTTATCTGTGTGAACGACAAAGAAACGCCACAAATCTGATAGTAT 877
Dbb 301 AGAAATTCAGATCAATTTATCTGTGTGAACGACAAAGAAACGCCACAAATCTGATAGTAT 360
QY 878 TTCCTTTCTTTGATGAAGCCCTGGCTCTGTGTGTAATAAGGAGATATTTGTGAAG 937
Dbb 361 TTCCTTTCTTTGATGAAGCCCTGGCTCTGTGTGTAATAAGGAGATATTTGTGAAG 420
QY 938 AAGCAGTAGCAGTGAATCTACAGGAGCCCATCGAATCCGGATCTTGTGCTGTGTAAG 997
Dbb 421 AAGCAGTAGCAGTGAATCTACAGGAGCCCATCGAATCCGGATCTTGTGCTGTGTAAG 480
QY 998 TGAACATTCAGGTGATTTGGTGGATCAGGATTCAGTTTCAGATCAGTTTGTAGTAATT 1057
Dbb 481 TGAACATTCAGGTGATTTGGTGGATCAGGATTCAGTTTCAGATCAGTTTGTAGTAATT 540
QY 1058 TGAAGTTCAATCTCTCGACTCAGAAAGATTATA 1089
Dbb 541 TGAAGTTCAATCTCTCGACTCAGAAAGATTATA 572

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RESULT 11
LOCUS BE300019 964 bp mRNA linear EST 20-JUL-2000
DEFINITION 600944138F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960385 5',
mRNA sequence.
ACCESSION BE300019
VERSION BE300019.1 GI:9183767
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 964)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

```

```

Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
Plate: L1CM53 row: k column: 10
High quality sequence stop: 688.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2960385"
/clone_lib="NIH_MGC_17"
/tissue_type="Rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 309 a 219 c 238 g 198 t
ORIGIN
Query Match 22.6% Score 535.2; DB 10; Length 964;
Best Local Similarity 90.8%; Pred. No. 1.1e-91;
Matches 739; Conservative 0; Mismatches 53; Indels 22; Gaps 15;

QY 28 GCCTGTGTGGCCCTGTGTGTC-GGAAAGATGGAGCAAGAGCGGAGCGGCGGCGGC 85
Dbb 1 GCCTGTGTGGCCCTGTGTGTCGGAAAGATGGAGCAAGAGCGGAGCGGCGGCGGC 59
QY 87 CGCGACCCCTCGACCGAGATCTCTGCTTCGACGCCA-GGAGCACCTCTCCCTCCC- 144
Dbb 60 CGCGACCCCTCGACCGAGATCTCTGCTTCGACGCCAAGAGCGGAGCGGCGGCGGC 119
QY 145 GGATTAGTTCGTACGAGCGCCAGTCGCCCTGGCCGGAGAGTGGAAATGATCCCGGAGGCC 204
Dbb 120 GGATTAGTTCGTACGAGCGCCAGTCGCCCTGGCCGGAGAGTGGAAATGATCCCGGAGGCC 179
QY 205 CAGGGCGTCTGCTTCGCGAGTAGTACGTCGCCCTGAGGAAACTGGGAGTCTTTCAGGG 264
Dbb 180 CAGGGCGTCTGCTTCGCG-----CGCGCCCTGAGGAAACTGGGAGTCTTTCAGGG 232
QY 265 ACCCGCGACTCCCAAGCGGAAACCCCGGATGGTGAGGAGCAGGCAAAATGTCAATACCA 324
Dbb 233 ACCCGCGACTCCCAAGCGGAAACCCCGGATGGTGAGGAGCAGGCAAAATGTCAATACCA 292
QY 325 ACATGCTGTACTACTGATGGTGTACCACTCAGAGATTCAGGTTCCAGTTCGGACAAAG 384
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QY 385 AGACCTGTGTAGACCAAGCCATTGCTTTTGAAGTATTATAAGTCTGTGG-TGCACAA 443
Dbb 353 AGACCTGTGTAGACCAAGCCATTGCTTTTGAAGTATTATAAGTCTGTGGTTGTCACAA 412
QY 444 AAAGACACTTATCTATGAAAGAGGTCTTTTATCTTGGCCAGTATATATGACTATAA 503
Dbb 413 AAAGACACTTATCTATGAAAGAGGTCTTTTATCTTGGCCAGTATATATGACTATAA 472
QY 504 CGATTATATGATGAGAAGC-AACAACATATTGTATTGTT-CAAAATGATCTTCTAGGAG 561
Dbb 473 CGATTATATGATGAGAAGCAACAACATATTGTATTGTTTACAAATGATCTTCTAGGAG 532
QY 562 ATTTGT-TTGGCGTCCCAAGCTTCTGTGAAAGAGCAGCAAGAAATATATATACCATGATC 620
Dbb 533 ATTTGTAAAGCGTCCCAAGCTTCTGTGAAAGAGCAGCAAGAAATATATATACCATGATC 592
QY 621 TACAGGAACCTTGGTA-GTAGTCAATCAGCAGGAA-TCATCGGACTCAGGTACA-TCTGTG 677

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Db 593 TACAGGAAGTGGTAGTCAATACACGAGAACTCATCGGACTCAGGTACACTCTGTG 652
Qy 678 AG-TGAGAACAGGTGTCACCTTGAAGTGGAGTGCATCAAAAGGACCTTGTACAGAGCT 736
Db 653 AGTTGAGAACAGCGTGTACCTTTGAGGTGGAGTGCATCGAAAGAC--TTGTACAGAGCT 710
Qy 737 TCAGGAAGAAACCTTTCATCTTTCACATTTGGTTTCTAGACCATCTACCTCACTCACTAACAA 796
Db 711 TCAGGAAGAGACACCTCATCTACACA--TTGGTATCAGAACATCTACCTCACTCACTAACAA 769
Qy 797 GAGAGCAATAGTGAGACAGAGAAATTCAGAT 830
Db 770 GAGAGCATAGTGAGACGAGAGAAATGAGATGAT 803

RESULT 12
BQ672178 847 bp mRNA linear EST 15-JUL-2002
LOCUS AGENCOURT_8301947 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275047
DEFINITION 5', mRNA sequence.
ACCESSION BQ672178
VERSION BQ672178.1 GI:21783012
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE NIH-MGC http://mgc.ncl.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2457 row: j column: 08
High quality sequence stop: 485.
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/lab_host="DH10B (phage-resistant)"
/site="organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 196 a 218 c 246 g 186 t 1 others
ORIGIN

Query Match 22.4%; Score 530.6; DB 14; Length 847;
Best Local Similarity 97.7%; Pred. No. 8.1e-91;
Matches 561; Conservative 0; Mismatches 5; Indels 8; Gaps 2;

Qy 8 CGCAGCTTGCTCTCTGGGCGCTGTGGCCCTGTGTGCGAAAGATGGACGAAGAA 67
Db 14 GCGAGCTTGCTCTCTGGGCGCTGTGTGGCCCTGTGTGCGAAAGATGGACGAAGAA 73
Qy 68 GCGAGCGCCGAGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTCGAGCCAG 127
Db 74 GCGAGCGCCGAGGGCGCGGACCCCTCTGACCGAGATCCTGCTGCTTCGAGCCAG 133

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Qy 128 GAGCACCCTCCCTCCCGGATTAGTGGCTAGCAGCGCCAGTGCCTTGGCCCGGAGAGTG 187
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Qy 188 GAATGATCCCGGAGGCGCCAGGCGCTGCTTCCGCGAGTAGTCAGTCCCGCGTGAAGGAAA 247
Db 194 GAATGATCCCGGAGGCGCCAGGCGCTGCTTCCG-----CGCGCCCGCTGAAGGAAA 246
Qy 248 CTGGGAGTCTTGGAGGAGCCCGGACTCCAGCGCGGAAACCCGCGATGGTGGAGGAGAG 307
Db 247 CTGGGAGTCTTGGAGGAGCCCGGACTCCAGCGCGGAAACCCGCGATGGTGGAGGAGAG 306
Qy 308 GCAATGTGCAATACCAACATGCTGTACTACTGCTGTGCTGTGTGTGTGTGTGTGTGTGT 367
Db 307 GCAATGTGCAATACCAACATGCTGTACTACTGCTGTGTGTGTGTGTGTGTGTGTGTGT 366
Qy 368 TCCAGCTTCGGAGACAGAGACCTGTTAGACCAAGCCATGCTTTGAAGTTATTAA 427
Db 367 TCCAGCTTCGGAGACAGAGACCTGTTAGACCAAGCCATGCTTTGAAGTTATTAA 426
Qy 428 GTCTGTGGTGCACAAAAAGACACTTATATATATGAAAGAGGTTCTTTTATCTTGGCCA 487
Db 427 GTCTGTGGTGCACAAAAAGACACTTATATATGAAAGAGGTTCTTTTATCTTGGCCA 486
Qy 488 GTATATATGACTAAACGATTATATGATGAGAGCAACACATATTGTATATTGTTCAA 547
Db 487 GTATATATGACTAAACGATTATATGATGAGAGCAACACATATTGTATATTGTTCAA 546
Qy 548 TGATCTCTAGGAGA-TTTGTTTGGCGTGGCCAAG 580
Db 547 TGATCTCTAGGAGATTTTGTGTTGGCGTGGCCAAG 580

RESULT 13
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LOCUS CIT-HSP-2361114.TR CIT-HSP Homo sapiens genomic clone 2361114, DNA
DEFINITION sequence.
ACCESSION AQ077720
VERSION AQ077720.1 GI:3438904
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
JOURNAL Map Building
COMMENT Unpublished (1998)
Other_GSSs: CIT-HSP-2361114.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamas@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
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Best Local Similarity 98.9%; Pred. No. 5.5e-90;
Matches 530; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1457 TACACAGCTTCACAAATCACAAGAGTGAAGACTATTCTCAGCCATCAACTTCTAGTAG 1516
Db 2 TACTCAGCTTACATACACAGAAAGTGNAGACTATTCTCAGCCATCAACTTCTAGTAG 61

Qy 1517 CATATTATTATAGCAGCCAGCAAGAGTGAAGAGTTTGAAGGGGAAGAAACCCCAAGACAA 1576
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Qy 1577 AGAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCGATTGAACCTTGTGTGATTGTCA 1636
Db 122 AGAAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCGATTGAACCTTGTGTGATTGTCA 181

Qy 1637 AGGTGACCTAAATAAGTGGTTCATTTGCCATGGCAAAACAGACATCTTATGGCTGCTT 1696
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Qy 1697 TACATGTGCAAGAGAGTGAAGAAAGGAATGAAGCCCTGCCAGTATGTAGACAAACCAAT 1756
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Qy 1757 TCAATGATGTGCTAATCTATTTCCTAGTTGACCTGCTCTATAGAGAATTTATATAT 1816
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Qy 1817 TCTAATGATGATGACCTGACAAATTTAGCAACCTGAATTTATTCACATATATCAAGTG 1876
Db 362 TCTAATGATGATGACCTGACAAATTTAGCAACCTGAATTTATTCACATATATCAAGTG 421

Qy 1877 AGAAATGCTCAATCACAATAGATTTCTCTCTTTAGTATTAATTTGACCTACTTTGGTAG 1936
Db 422 AGAAATGCTCAATCACAATAGATTTCTCTCTTTAGTATTAATTTGACCTACTTTGGTAG 481

Qy 1937 TGGATAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1992
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RESULT 14
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LOCUS 601176992F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532102 5',
DEFINITION mRNA sequence.
ACCESSION BE296905
VERSION BE296905.1 GI:9180472
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL 1 (bases 1 to 555)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM207 row: h column: 23
High quality sequence stop: 543.

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/clone_lib="NIH_MGC_17"
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/notes="Organ: muscle; Vector: pOB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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BASE COUNT 133 a 141 c 156 g 125 t
ORIGIN

Query Match 21.9%; Score 519; DB 10; Length 555;
Best Local Similarity 97.7%; Pred. No. 1.4e-88;
Matches 550; Conservative 0; Mismatches 5; Indels 8; Gaps 2;

Qy 16 GGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAGATGGAGCAAGCCGAGCC 75
Db 1 GGCTCTTCTGGGCGCTGTGTGGCCCTGTGTGCGGAAGATGGAGCAAGCCGAGCC 60

Qy 76 CGAGGGCGCGCGGACCCCTCTGACCGAGATCTGCTGCTTTCGCGAGCAGGACCG 135
Db 61 CGAGGGCGCGCGGACCCCTCTGACCGAGATCTGCTGCTTTCGCGAGCAGGACCG 120

Qy 136 TCCCTCCCGGATAGTGCGTACGAGCCGCGGCGGCGGCGGAGAGTGAATGATC 195
Db 121 TCCCTCCCGGATAGTGCGTACGAGCCGCGGCGGCGGAGAGTGAATGATC 180

Qy 196 CCGAGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 255
Db 181 CCGAGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 233

Qy 256 TCTTGGAGGACCCCGGACTCCAAGCGGCAAAACCCCGGATGGTGAGGAGCAGCAATGT 315
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Qy 316 GCAATACCAACATGCTGTACTTACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 375
Db 294 GCAATACCAACATGCTGTACTTACTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 353

Qy 376 CGGAACAAGAGACCCCTGGTTAGACCAAGCCATTCGCTTTTGAAGTTATTAAGTCTGTTG 435
Db 354 CGGAACAAGAGACCCCTGGTTAGACCAAGCCATTCGCTTTTGAAGTTATTAAGTCTGTTG 413

Qy 436 GTGCACAAAAGACACTTATATGAAAGAGGTTCTTTTATCTTGGCCAGTATATTA 495
Db 414 GTGCACAAAAGACACTTATATGAAAGAGGTTCTTTTATCTTGGCCAGTATATTA 473

Qy 496 TGACTAAACGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 555
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Qy 556 TAGGAGATTTGTTGGCGTGCCA 578
Db 534 TAGGAGATTTGTTGGCGTGCCA 555

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DEFINITION EST387557 MAGE resequences, MAGN Homo sapiens cDNA, mRNA sequence.
ACCESSION AW975448
VERSION AW975448.1 GI:8166661
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 674)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)

COMMENT Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: johnqu@tigr.org

Plate: 349

Seq primer: Forward.

FEATURES Location/Qualifiers

source

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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="MAGE resequences, MAGN"

/note="Vector: paluescriptskm"

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Best Local Similarity 81.4%; Pred. No. 1.5e-81;
Matches 658; Conservative 0; Mismatches 8; Indels 142; Gaps 3;
Qy 82 GCGGCCGCGACCCCTCTGACCGAGATCTGCTGCTTTGCGAGCAGGAGCAGCCGCTCCCTC 141
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Qy 142 CCGGATTAGTGGTACGAGCGCCAGTGCCTGCGCGGAGAGTGAATGATCCCGGAG 201
Db 67 CCGGATTAGTGGTACGAGCGCCAGTGCCTGCGCGGAGAGTGAATGATCCCGGAG 126
Qy 202 GCCCAGGGCGTCTGCTCGGAGTAGTACGTCCTGCGCGGAGAGTGAATGATCCCGGAG 261
Db 127 GCCCAGGGCGTCTGCTCGGAGTAGTACGTCCTGCGCGGAGAGTGAATGATCCCGGAG 179
Qy 262 GGGACCCCGACATCCCAAGCGCGAAACCCCGGATGGTGGAGCAGGCAAAATGTGCAATA 321
Db 180 GGGACCCCGACATCCCAAGCGCGAAACCCCGGATGGTGGAGCAGGCAAAATGTGCAATA 239
Qy 322 CCAACATGCTGTACTACTGATGGTGTGTACCCACCTCACAGATTCAGCTTCGGAC 381
Db 240 CCAACATGCTGTACTACTGATGGTGTGTACCCACCTCACAGATTCAGCTTCGGAC 299
Qy 382 AAGAGACCCCTGTTAGACCAAGCCATTGCTTTTGAAGTTATTAAGTCTGTGGTGCAC 441
Db 300 AAGAGACCCCTGTTAGACCAAGCCATTGCTTTTGAAGTTATTAAGTCTGTGGTGCAC 359
Qy 442 AAAAGACACTTATATCTATGAAGAGGTTCTTTTATCTTGGCCAGTATATTATGACTA 501
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Qy 502 AACGATTATATGATGAGAGCAACACATATGTATATTTGTCAAAATGATCTTAGGAG 561
Db 384 ----- 383
Qy 562 ATTTGTTTGGCGTCCCAAGCTTCTCTGTGAAAGAGCAGCAAGAAATATATACCATGATCT 621
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Qy 622 ACAGGAACCTTGTAGTAGTCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTG 681
Db 406 ACAGGAACCTTGTAGTAGTCAATCAGCAGGAATCATCGGACTCAGGTACATCTGTGAGTG 465
Qy 682 AGAAGAGGCTGTCACCTTGAAGTGGGAGTGATCAAAAGGACCTTGTACAGAGCTTCAGG 741
Db 466 AGAAGAGGCTGTCACCTTGAAGTGGGAGTGATCAAAAGGACCTTGTACAGAGCTTCAGG 525

Qy 742 AAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCATCTACCTCATCTAGAGGAGAG 801
Db 526 AAGAGAAACCTTCATCTTCACATTTGGTTTCTAGACCATCTACCTCATCTAGAGGAGAG 585
Qy 802 CAATTAGTGAGACAGAGAAGAAATTCAGATGAATTTATCTGGTGAACGACAAAGAAAACGCC 861
Db 586 CAATTAGTGAGACAGAGAAG-AAATTCAGATGAATTTATCTGGTGAACGACAAAGAAAACGCC 644
Qy 862 ACAATCTGATAGTATTTCCCTTTCCTT 889
Db 645 ACAATCTGATAGATTTCCCTTTCCTT 672

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Job time : 3342 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2003, 11:00:44 ; Search time 107 Seconds
(without alignments)
9756.310 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcaccgcgcagcttgctg.....attacaggcatgaccacgc 2372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 389086 seqs, 220051671 residues 778172

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA.*

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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
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| 2 | 2372 | 100.0 | 2372 | 10 | US-09-956-425-7 |
| 3 | 2372 | 100.0 | 2372 | 10 | US-09-851-771A-1 |
| 4 | 975.6 | 41.1 | 1710 | 10 | US-09-956-425-5 |
| 5 | 652 | 27.5 | 652 | 12 | US-10-057-510-3 |
| 6 | 226.4 | 9.5 | 148567 | 10 | US-09-801-8768-3 |
| 7 | 226 | 9.5 | 1400 | 10 | US-09-263-959-295 |
| 8 | 226 | 9.5 | 684973 | 10 | US-09-764-869-2355 |
| 9 | 223.2 | 9.4 | 22008 | 10 | US-09-764-869-2110 |
| 10 | 223.2 | 9.4 | 32185 | 10 | US-09-764-877-3171 |
| 11 | 223 | 9.4 | 4978 | 10 | US-09-764-877-335 |
| 12 | 222 | 9.4 | 13608 | 10 | US-09-861-846-3 |
| 13 | 222 | 9.4 | 41104 | 10 | US-09-816-685-3 |
| 14 | 221.8 | 9.4 | 15714 | 10 | US-09-764-869-2355 |
| 15 | 221.8 | 9.4 | 32190 | 10 | US-09-764-878-201 |
| 16 | 221.8 | 9.4 | 32193 | 10 | US-09-764-878-200 |
| 17 | 221.8 | 9.4 | 32249 | 10 | US-09-764-878-202 |
| 18 | 221.4 | 9.3 | 32174 | 9 | US-09-860-670-232 |
| 19 | 221.4 | 9.3 | 32174 | 9 | US-09-764-904-90 |

ALIGNMENTS

RESULT 1

US-09-752-983-1

Sequence 1, Application US/09752983

Patent No. US20010016575A1

GENERAL INFORMATION:

APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.

APPLICANT: Graham, Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2

TITLE OF INVENTION: EXPRESSION

NUMBER OF INVENTIONS: 271

CORRESPONDENCE ADDRESS:

ADDRESSER: Law Offices of Jane Massey Licata

STREET: 66 East Main Street

CITY: Marlton

STATE: NJ

COUNTRY: U.S.A.

ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM PC

OPERATING SYSTEM: WINDOWS 95

SOFTWARE: WORDPERFECT 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09752,983

FILING DATE: 02-Jan-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/280,805

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Licata, Jane Massey

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0346

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-810-1515

TELEFAX: 609-810-1454

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Unknown

Sequence 158, App

Sequence 1134, Ap

Sequence 2645, Ap

Sequence 183, App

Sequence 224, App

Sequence 199, App

Sequence 11, Appl

Sequence 132, Ap

Sequence 1, Appli

Sequence 1, Appli

Sequence 226, App

Sequence 217, App

Sequence 11, Appl

Sequence 1541, Ap

Sequence 1546, Ap

Sequence 1543, Ap

Sequence 1544, Ap

Sequence 7, Appli

Sequence 3, Appli

Sequence 609, App

Sequence 163, App

Sequence 1849, Ap

Sequence 3, Appli

Sequence 3, Appli

ANTI-SENSE: No
 PUBLICATION INFORMATION:
 AUTHORS: Olinier, J. D.
 AUTHORS: Kinzler, K. W.
 AUTHORS: Meltzer, P. S.
 AUTHORS: George, D. L.
 AUTHORS: Vogelstein, B.
 TITLE: Amplification of a gene encoding a
 JOURNAL: Nature
 VOLUME: 358
 ISSUE: 6381
 PAGES: 80-83
 DATE: 02-JUL-1992
 US-09-752-983-1

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| Db 1 | GCACCGCGAGCTTGGCTGCTTCTGGGGCTGTGTGGCCCTGTGTGGGAGATGGA | 60 | | | | | | | |
| Qy 61 | GCAAGAACCGAGCCGAGGGCGCGCCGACCCCTCTGACGAGATCTGTGCTTTCG | 120 | | | | | | | |
| Db 61 | GCAGAGCGAGCCGAGGGCGCGCCGACCCCTCTGACGAGATCTGTGCTTTCG | 120 | | | | | | | |
| Qy 121 | CAGCCAGGAGCACCCTCCCGGATAGTGGGTACGAGCGCCGAGTGGCCCTGGCCCG | 180 | | | | | | | |
| Db 121 | CAGCCAGGAGCACCCTCCCGGATAGTGGGTACGAGCGCCGAGTGGCCCTGGCCCG | 180 | | | | | | | |
| Qy 181 | GAGAGTGGAAATGATCCCGAGGCCGAGGGCTGTGCTTCCGAGTACGAGTCCCGTG | 240 | | | | | | | |
| Db 181 | GAGAGTGGAAATGATCCCGAGGCCGAGGGCTGTGCTTCCGAGTACGAGTCCCGTG | 240 | | | | | | | |
| Qy 241 | AAGAAATCGGGAGTCTTGAGGACCCCGGACTCCAGCGGAGAAACCCCGGATGGA | 300 | | | | | | | |
| Db 241 | AAGAAATCGGGAGTCTTGAGGACCCCGGACTCCAGCGGAGAAACCCCGGATGGA | 300 | | | | | | | |
| Qy 301 | GGAGCGGCAATGCAATACCAACATGTCTGCTACTGATGAGTGTGTAAACCACT | 360 | | | | | | | |
| Db 301 | GGAGCGGCAATGCAATACCAACATGTCTGCTACTGATGAGTGTGTAAACCACT | 360 | | | | | | | |
| Qy 361 | CACAGATCCAGCTCGGAACAGAGACCTGTGTAGCCAAAGCCATTTGGAAGT | 420 | | | | | | | |
| Db 361 | CACAGATCCAGCTCGGAACAGAGACCTGTGTAGCCAAAGCCATTTGGAAGT | 420 | | | | | | | |
| Qy 421 | TATTAAGTCTGTGTGCAACAAAGACACTTATATCTATGAAAGAGTCTTTTATC | 480 | | | | | | | |
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| Qy 541 | GTTCAGATCTGTAGGAGATTTGTGGCGGCCAGCTCTCTGTGAAAGAGCACA | 600 | | | | | | | |
| Db 541 | GTTCAGATCTGTAGGAGATTTGTGGCGGCCAGCTCTCTGTGAAAGAGCACA | 600 | | | | | | | |
| Qy 601 | GGAAATATATACCATGATCTACAGGAACCTTGTGTAGTGTGATGAGGAGTATCGG | 660 | | | | | | | |
| Db 601 | GGAAATATATACCATGATCTACAGGAACCTTGTGTAGTGTGATGAGGAGTATCGG | 660 | | | | | | | |
| Qy 661 | ACTCAGTACATCTGTAGTGTAGGAGGAGTGTACCTTGAAGTGGAGTGTCAAAAGG | 720 | | | | | | | |
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| Qy 721 | ACCTTGTACAGAGCTTCAGGAGAGAACCTTCATCTCAGATTTGGTTCTAGACCAT | 780 | | | | | | | |
| Db 721 | ACCTTGTACAGAGCTTCAGGAGAGAACCTTCATCTCAGATTTGGTTCTAGACCAT | 780 | | | | | | | |
| Qy 781 | CTACCTCATCTAGAGGAGCAATTAGTGAGACAGAGAAATTCAGATGATATCTG | 840 | | | | | | | |

| | | | | | | | | | |
|---------|---|------|--|--|--|--|--|--|--|
| Db 781 | CTACCTCATCTAGAGGAGCAATTAGTGAGACAGAGAAATTCAGATGATATCTG | 840 | | | | | | | |
| Qy 841 | GTGAACGACAAAGAACCCACAACTCTGATAGTATTTCCCTTTCTTTGATGAAGCC | 900 | | | | | | | |
| Db 841 | GTGAACGACAAAGAACCCACAACTCTGATAGTATTTCCCTTTCTTTGATGAAGCC | 900 | | | | | | | |
| Qy 901 | TGGCTCTGTGTGTAATAAGGGAGATATCTTGTGAAGAACAGCAGTAGCAGTGAATC | 960 | | | | | | | |
| Db 901 | TGGCTCTGTGTGTAATAAGGGAGATATCTTGTGAAGAACAGCAGTAGCAGTGAATC | 960 | | | | | | | |
| Qy 961 | GGACGCCATCGAATCCGGATCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1020 | | | | | | | |
| Db 961 | GGACGCCATCGAATCCGGATCTTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG | 1020 | | | | | | | |
| Qy 1021 | ATCAGGATTCAGTTTCAGATCAGTTTCTGATGATGATGATGATGATGATGATGATG | 1080 | | | | | | | |
| Db 1021 | ATCAGGATTCAGTTTTCAGATCAGTTTCTGATGATGATGATGATGATGATGATGATG | 1080 | | | | | | | |
| Qy 1081 | AAGATTATAGCCCTTAGTGAAGAACCAAGAACTCTCAGATGAAGATGATGAGGTATATC | 1140 | | | | | | | |
| Db 1081 | AAGATTATAGCCCTTAGTGAAGAACCAAGAACTCTCAGATGAAGATGATGAGGTATATC | 1140 | | | | | | | |
| Qy 1141 | AAGTTACTGTGTATCAGGAGGAGAGTGTACAGATTTCAATTTGAAGAGATCTCTGAAA | 1200 | | | | | | | |
| Db 1141 | AAGTTACTGTGTATCAGGAGGAGAGTGTACAGATTTCAATTTGAAGAGATCTCTGAAA | 1200 | | | | | | | |
| Qy 1201 | TTTCTTAGTCTGATTTGGAAATGCATCTCATGATGAATGAATCCGCCCTTCCAT | 1260 | | | | | | | |
| Db 1201 | TTTCTTAGTCTGATTTGGAAATGCATCTCATGATGAATGAATCCGCCCTTCCAT | 1260 | | | | | | | |
| Qy 1261 | CACATTGCAACAGATTTGGGCCCTTCTGTGAGATTTGGCTTCTGAGAGATAAGGGAAG | 1320 | | | | | | | |
| Db 1261 | CACATTGCAACAGATTTGGGCCCTTCTGTGAGATTTGGCTTCTGAGAGATAAGGGAAG | 1320 | | | | | | | |
| Qy 1321 | ATAAGGGGAAATCTCTGAGAGGAGCAAACTTGAAGAACTCAACAGCTGAGAGGCT | 1380 | | | | | | | |
| Db 1321 | ATAAGGGGAAATCTCTGAGAGGAGCAAACTTGAAGAACTCAACAGCTGAGAGGCT | 1380 | | | | | | | |
| Qy 1381 | TTGATGTTCTGATTTGAAAAAACTATAGTGAATGATTTCCAGAGAGTCAATGTTGAGG | 1440 | | | | | | | |
| Db 1381 | TTGATGTTCTGATTTGAAAAAACTATAGTGAATGATTTCCAGAGAGTCAATGTTGAGG | 1440 | | | | | | | |
| Qy 1441 | AAATGATGATAAAATTCACAAAGCTTCAATCACAAGAAAGTGAAGACTATTTCTCAGC | 1500 | | | | | | | |
| Db 1441 | AAATGATGATAAAATTCACAAAGCTTCAATCACAAGAAAGTGAAGACTATTTCTCAGC | 1500 | | | | | | | |
| Qy 1501 | CATCACTTCTAGTACATTTATAGCAGCAGAGAGATGTGABAGACTTTGAAGG | 1560 | | | | | | | |
| Db 1501 | CATCACTTCTAGTACATTTATAGCAGCAGAGAGATGTGABAGACTTTGAAGG | 1560 | | | | | | | |
| Qy 1561 | AAGAAACCCAGAACAAAGAGAGAGTGGAACTAGTTTGGCCCTTAATGCAATTTGAAC | 1620 | | | | | | | |
| Db 1561 | AAGAAACCCAGAACAAAGAGAGAGTGGAACTAGTTTGGCCCTTAATGCAATTTGAAC | 1620 | | | | | | | |
| Qy 1621 | CTTCTGTGATTTCTCAAGCTCGACCTTAAATTTGTTGCTTCATGCGCAAAACAGGAC | 1680 | | | | | | | |
| Db 1621 | CTTCTGTGATTTCTCAAGCTCGACCTTAAATTTGTTGCTTCATGCGCAAAACAGGAC | 1680 | | | | | | | |
| Qy 1681 | ATCTTATGGCTGCTTTACATGTGCAAGAGAGCTTAAGAAAGGAATTAAGCCCTGCCAG | 1740 | | | | | | | |
| Db 1681 | ATCTTATGGCTGCTTTACATGTGCAAGAGAGCTTAAGAAAGGAATTAAGCCCTGCCAG | 1740 | | | | | | | |
| Qy 1741 | TATGTAGCAACCAATTTCAATGATTTGCTAACTTATTTCCCTAGTTGACCTGTCTAT | 1800 | | | | | | | |
| Db 1741 | TATGTAGCAACCAATTTCAATGATTTGCTAACTTATTTCCCTAGTTGACCTGTCTAT | 1800 | | | | | | | |
| Qy 1801 | AAGAGATTTATATTTCTTCAACTATATTAACCTTAGAATTTAGACACCTGAATTTAT | 1860 | | | | | | | |
| Db 1801 | AAGAGATTTATATTTCTTCAACTATATTAACCTTAGAATTTAGACACCTGAATTTAT | 1860 | | | | | | | |
| Qy 1861 | CACATATATCAAGTGGAGAAATGCTTCAATTCACATAGATTTCTTCTTTAGTATAT | 1920 | | | | | | | |

Qy 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAAACTCAACACAGCTGAAGAGGCT 1380
 Db 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAAACTCAACACAGCTGAAGAGGCT 1380
 Qy 1381 TTGATGTTCTGATGTTAAAGAACTATAGTGAATGATCCAGAGATCATGTTGAGG 1440
 Db 1381 TTGATGTTCTGATGTTAAAGAACTATAGTGAATGATCCAGAGATCATGTTGAGG 1440
 Qy 1441 AAAATGATGATAAAATACAAAGCTTCACAAATCAACAAGAAAGTGAAGACTATTCTCAGC 1500
 Db 1441 AAAATGATGATAAAATACAAAGCTTCACAAATCAACAAGAAAGTGAAGACTATTCTCAGC 1500
 Qy 1501 CATCAACTTCTAGTAGCATTTATATAGCAGCCAAAGAAAGTGAAGAGTTTGAAGGG 1560
 Db 1501 CATCAACTTCTAGTAGCATTTATATAGCAGCCAAAGAAAGTGAAGAGTTTGAAGGG 1560
 Qy 1561 AGAAACCCCAAGCAAGAGAGTGTGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
 Db 1561 AGAAACCCCAAGCAAGAGAGTGTGAATCTAGTTGGCCCTTAATGCCATTGAAC 1620
 Qy 1621 CTTGTGTGATTTGTCAAGGTGACCTAAAATGGTTGCAATTTGCCATTTGCCAAACAGGAC 1680
 Db 1621 CTTGTGTGATTTGTCAAGGTGACCTAAAATGGTTGCAATTTGCCATTTGCCAAACAGGAC 1680
 Qy 1681 ATCTTATGCGCTTTTACATGTCGAAGAGCTTAAGAAAGGATAGCCCTGCCAG 1740
 Db 1681 ATCTTATGCGCTTTTACATGTCGAAGAGCTTAAGAAAGGATAGCCCTGCCAG 1740
 Qy 1741 TATGTAGAACCAATCAAAATGATGTGTAATTTATTTCCCTAGTTGACCTGCTAT 1800
 Db 1741 TATGTAGAACCAATCAAAATGATGTGTAATTTATTTCCCTAGTTGACCTGCTAT 1800
 Qy 1801 AAGAGAAATATATATTTCTAATATATAACCTAGGAATTTAGAACACCTGAAATTTAT 1860
 Db 1801 AAGAGAAATATATATTTCTAATATATAACCTAGGAATTTAGAACACCTGAAATTTAT 1860
 Qy 1861 CACATATATCAAGTGAAGAAATGCCCAATTCACATAGATTTCTTCTTTAGTATAT 1920
 Db 1861 CACATATATCAAGTGAAGAAATGCCCAATTCACATAGATTTCTTCTTTAGTATAT 1920
 Qy 1921 TGACCTACTTTGCTAGTGAATAGTGAATTTACTATAATTTGACTTGAATATGACT 1980
 Db 1921 TGACCTACTTTGCTAGTGAATAGTGAATTTACTATAATTTGACTTGAATATGACT 1980
 Qy 1981 CATCTTTTACACCACTCTTAATTTTAAATATTTCTACTCTCTTAAATGAGAATAC 2040
 Db 1981 CATCTTTTACACCACTCTTAATTTTAAATATTTCTACTCTCTTAAATGAGAATAC 2040
 Qy 2041 TTGGTTTTTTTTTCTTAATATGATGACATTTAAATGTAATTTATTTTATTTT 2100
 Db 2041 TTGGTTTTTTTTTCTTAATATGATGACATTTAAATGTAATTTATTTTATTTT 2100
 Qy 2101 AGACCGAGTCTTCTGTTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Db 2101 AGACCGAGTCTTCTGTTACCCAGGCTGGAGTGCAGTGGGTGATCTTGGCTCACTGCA 2160
 Qy 2161 AGCTCTGCCCTCCCGGGTTCGACATTCCTGCTGAGCTCCCAATTAAGCTTGGCC 2220
 Db 2161 AGCTCTGCCCTCCCGGGTTCGACATTCCTGCTGAGCTCCCAATTAAGCTTGGCC 2220
 Qy 2221 TACAGTCAATGCGCACCAACCTGGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTC 2280
 Db 2221 TACAGTCAATGCGCACCAACCTGGCTAAATTTTGTACTTTTGTAGTAGACAGGGTTTC 2280
 Qy 2281 ACCGTGTTAGCCAGGATGCTCTGATCTCCGACCTCGATCGCTGATCCGCCCTGCCCTCC 2340
 Db 2281 ACCGTGTTAGCCAGGATGCTCTGATCTCCGACCTCGATCGCTGATCCGCCCTGCCCTCC 2340
 Qy 2341 CAAAGTCTGGGATTAACAGGCAATGAGCACCG 2372
 Db 2341 CAAAGTCTGGGATTAACAGGCAATGAGCACCG 2372

RESULT 3
 US-09-851-771A-1
 : Sequence 1, Application US/09851771A
 : Patent No. US20020151511A1
 : GENERAL INFORMATION:
 : APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
 : : Graham, Brett P. Monla
 : TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
 : : MODULATION OF HUMAN MDM2 EXPRESSION
 : NUMBER OF SEQUENCES: 32
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Law Offices of Jane Massey Licata
 : STREET: 66 East Main Street
 : CITY: Marlton
 : STATE: NJ
 : COUNTRY: U.S.A.
 : ZIP: 08053
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 : COMPUTER: IBM 486
 : OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
 : SOFTWARE: WORDPERFECT 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/851,771A
 : FILING DATE: 09-May-2001
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/048,810
 : FILING DATE: 1998-03-26
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Licata, Jane Massey
 : REGISTRATION NUMBER: 32,257
 : REFERENCE/DOCKET NUMBER: ISPH-0302
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 609-779-2400
 : TELEFAX: 609-810-1454
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2372 base pairs
 : TYPE: Nucleic Acid
 : STRANDEDNESS: Single
 : TOPOLOGY: Unknown
 : ANTI-SENSE: No
 : PUBLICATION INFORMATION:
 : AUTHORS: Oliner, J.D., Kinzler, K.W., Meltzer, P.S., George, D.L., Vogelstein, B.
 : TITLE: Amplification of a gene encoding a p53-associated protein in
 : JOURNAL: Nature
 : VOLUME: 358
 : ISSUE: 6381
 : PAGES: 80-83
 : DATE: 02-JUL-1992
 : SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 : US-09-851-771A-1
 : Query Match 100.0%; Score 2372; DB 10; Length 2372;
 : Best Local Similarity 100.0%; Pred. No. 0;
 : Matches 2372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 : QY 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGGCCCTGTGTGTCGGAAGATGGA 60
 : DB 1 GCACCGCGCGAGCTTGGCTGCTTCTGGGGCCCTGTGTGTCGGAAGATGGA 60
 : QY 61 GCAAGAAAGCCGAGCCGCGAGGGCGCGACCCCTCTGACCGAGATCCCTGCTGCTTTCG 120
 : DB 61 GCAAGAAAGCCGAGCCGCGAGGGCGCGACCCCTCTGACCGAGATCCCTGCTGCTTTCG 120
 : QY 121 CAGCCAGGACCGCTCCCTCCCGGATTTAGTACGAGCCGCGAGTCCCTGCTGCTGCTG 180
 : DB 121 CAGCCAGGACCGCTCCCTCCCGGATTTAGTACGAGCCGCGAGTCCCTGCTGCTGCTG 180
 : QY 181 GAGAGTGAATGATCCCGAGGCCCGAGGGCGTGTGCTTCGCGAGTAGTCAGTCCCGCTG 240
 : DB 181 GAGAGTGAATGATCCCGAGGCCCGAGGGCGTGTGCTTCGCGAGTAGTCAGTCCCGCTG 240

Db 181 GAGGTGGAAATGATCCCGAGGCCCGGCGTCTCCCGAGTAGCTAGTCCCGCGTG 240
Qy 241 AAGGAACTGGGGAGTCTTGAGGAGCCCCGAGCTCCAGCGGGAAGACCCCGGATGTGA 300
Db 241 AAGGAACTGGGGAGTCTTGAGGAGCCCCGAGCTCCAGCGGGAAGACCCCGGATGTGA 300
Qy 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACTACTACTGATGGTCTGTAAACACCT 360
Db 301 GGAGCAGGCAATGTGCAATACCAACATGTCTGTACTACTACTGATGGTCTGTAAACACCT 360
Qy 361 CACAGATTCAGCTTCGGAACAGAGACCTGGTTAGACCAAGCAATGCTTTTGAAGT 420
Db 361 CACAGATTCAGCTTCGGAACAGAGACCTGGTTAGACCAAGCAATGCTTTTGAAGT 420
Qy 421 TATTAAGTCTGGTGCACAAAAGACACTTATACTATGAAGAGGTCTTTTTTATC 480
Db 421 TATTAAGTCTGGTGCACAAAAGACACTTATACTATGAAGAGGTCTTTTTTATC 480
Qy 481 TTGGCCAGTATATGACTAAAGCAATPATATGATGAGAGCAACACATATTTATTT 540
Db 481 TTGGCCAGTATATGACTAAAGCAATPATATGATGAGAGCAACACATATTTATTT 540
Qy 541 GTTCAAAATGATCTTAGGAGATTTGTTGGCGTGCCAAAGCTTCTCTGTGAAAGCACA 600
Db 541 GTTCAAAATGATCTTAGGAGATTTGTTGGCGTGCCAAAGCTTCTCTGTGAAAGCACA 600
Qy 601 GGAATATATACCATGATCTACAGGAACCTTGATAGTAGTCAATCAGCAGGAATCATCGG 660
Db 601 GGAATATATACCATGATCTACAGGAACCTTGATAGTAGTCAATCAGCAGGAATCATCGG 660
Qy 661 ACTCAGGTACATCTGTAGTGAGAACAGGTGTCAACCTTGAAGGTGGGAGTGAACAAAGG 720
Db 661 ACTCAGGTACATCTGTAGTGAGAACAGGTGTCAACCTTGAAGGTGGGAGTGAACAAAGG 720
Qy 721 ACCTTGTACAAGAGCTTCAGGAAGAAACCTTCATCTTCACATTTGGTTCTTAGACCAT 780
Db 721 ACCTTGTACAAGAGCTTCAGGAAGAAACCTTCATCTTCACATTTGGTTCTTAGACCAT 780
Qy 781 CTACCTCATCTAGAGGAGCAATTAGTGAGACAGAAATTCAGATGAATATCTG 840
Db 781 CTACCTCATCTAGAGGAGCAATTAGTGAGACAGAAATTCAGATGAATATCTG 840
Qy 841 GTGAACGACAAAGAAAGCCCAAAATCTGATAGTATTTCCCTTTCCCTTTGATGAAAGCC 900
Db 841 GTGAACGACAAAGAAAGCCCAAAATCTGATAGTATTTCCCTTTCCCTTTGATGAAAGCC 900
Qy 901 TGGCTCTGTGTATAAGGAGGATATGTTGTGAAGAAAGCAGTAGCAGTGAATCTACAG 960
Db 901 TGGCTCTGTGTATAAGGAGGATATGTTGTGAAGAAAGCAGTAGCAGTGAATCTACAG 960
Qy 961 GGAGCCATCGAATCCGATCTTGATCGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
Db 961 GGAGCCATCGAATCCGATCTTGATCGTGAAGTGAACATTCAGGTGATTTGGTGG 1020
Qy 1021 ATCAGGATTCAGTTTCAGATCAGTTTATGTAGAAATTTGAAGTTTGAATCTCTGACATCAG 1080
Db 1021 ATCAGGATTCAGTTTCAGATCAGTTTATGTAGAAATTTGAAGTTTGAATCTCTGACATCAG 1080
Qy 1081 AAGATTATAGCTTATGTAAGAGGACAAAGAACTCTCAGATGAATGATGAGGTATATC 1140
Db 1081 AAGATTATAGCTTATGTAAGAGGACAAAGAACTCTCAGATGAATGATGAGGTATATC 1140
Qy 1141 AAGTTACTGTATCAGCAGGAGAGTATACAGATTCATTTGAAGATCCTGAAA 1200
Db 1141 AAGTTACTGTATCAGCAGGAGAGTATACAGATTCATTTGAAGATCCTGAAA 1200
Qy 1201 TTTCCCTTAGCTATTTGGAATTCACATTCATGCAATGAATCCCCCCTTCCAT 1260
Db 1201 TTTCCCTTAGCTATTTGGAATTCACATTCATGCAATGAATCCCCCCTTCCAT 1260
Qy 1261 CACATTCGAACAGATTTGGGCCCTTCGTGAGAAATGGCTTCTGAAATGAAGGAAAG 1320
Db 1261 CACATTCGAACAGATTTGGGCCCTTCGTGAGAAATGGCTTCTGAAATGAAGGAAAG 1320

Qy 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAAAACTCAACACAGCTGAAGAGGGCT 1380
Db 1321 ATAAAGGGAAATCTCTGAGAAAGCCAAACTGGAAAACTCAACACAGCTGAAGAGGGCT 1380
Qy 1381 TTGATGTTCCCTGATTTGAAAAAATATAGTGAATGATTTCCAGAGAGTCAATGTTGAGG 1440
Db 1381 TTGATGTTCCCTGATTTGAAAAAATATAGTGAATGATTTCCAGAGAGTCAATGTTGAGG 1440
Qy 1441 AAAATGATGATAAATACACAAAGCTTCAATCAAGAAAGTGAAGACTATTTCTCAGC 1500
Db 1441 AAAATGATGATAAATACACAAAGCTTCAATCAAGAAAGTGAAGACTATTTCTCAGC 1500
Qy 1501 CATCAACTCTAGTAGCATTTATTTAGCAGCAAGAGATGTGAAGAGTTTGAAGGG 1560
Db 1501 CATCAACTCTAGTAGCATTTATTTAGCAGCAAGAGATGTGAAGAGTTTGAAGGG 1560
Qy 1561 AAGAAACCCAGACAAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
Db 1561 AAGAAACCCAGACAAAGAGAGAGTGTGGAATCTAGTTTGGCCCTTAATGCCATTTGAAC 1620
Qy 1621 CTTGTGTGATTTGTCAAAGTTCGACCTTAAANAATGGTTGCATTTCCATGGCAAAACAGGAC 1680
Db 1621 CTTGTGTGATTTGTCAAAGTTCGACCTTAAANAATGGTTGCATTTCCATGGCAAAACAGGAC 1680
Qy 1681 ATCTTATGGCCCTGCTTTACATGTGCAAGAGCTTAAAGAAAGNAATAGCCCTGGCCAG 1740
Db 1681 ATCTTATGGCCCTGCTTTACATGTGCAAGAGCTTAAAGAAAGNAATAGCCCTGGCCAG 1740
Qy 1741 TATGTAGAACCACTTCAATGATTTGCTAACTTATTTCCCTTAGTTGACCTGTCTAT 1800
Db 1741 TATGTAGAACCACTTCAATGATTTGCTAACTTATTTCCCTTAGTTGACCTGTCTAT 1800
Qy 1801 AAGAGAAATATATTTCTTAACATATATAACCTTAGGAATTTAGACAACCTGAAATTTATT 1860
Db 1801 AAGAGAAATATATTTCTTAACATATATAACCTTAGGAATTTAGACAACCTGAAATTTATT 1860
Qy 1861 CACATATACAAAGTGAAGAAAGCCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
Db 1861 CACATATACAAAGTGAAGAAAGCCCTCAATTCACATAGATTTCTCTCTTTAGTATAAT 1920
Qy 1921 TGACCTACTTTGGTAGTGGAAATAGTGAATCTACTTACTTAAATTTGACTTTGAATATGACT 1980
Db 1921 TGACCTACTTTGGTAGTGGAAATAGTGAATCTACTTACTTAAATTTGACTTTGAATATGACT 1980
Qy 1981 CATCTCTTACACCAACTCCTAAATTTAAATAATTTCTACTCTGCTTAAATGAGAAGTAC 2040
Db 1981 CATCTCTTACACCAACTCCTAAATTTAAATAATTTCTACTCTGCTTAAATGAGAAGTAC 2040
Qy 2041 TTGGTCTTTTCTTTTAAATATGATGATGACATTTAAATGTAACCTATTTATTTTCTTTC 2100
Db 2041 TTGGTCTTTTCTTTTAAATATGATGATGACATTTAAATGTAACCTATTTATTTTCTTTC 2100
Qy 2101 AGACGAGTCTTGTCTGTTTACCAGAGCTGGAGTGCAGTGGGTGATCTGGCTCACATGCA 2160
Db 2101 AGACGAGTCTTGTCTGTTTACCAGAGCTGGAGTGCAGTGGGTGATCTGGCTCACATGCA 2160
Qy 2161 AGCTCTGCCCTCCCGGGTTCGCACCACTTCTCTGCTCAGCCTCCCAATTTAGCTTGGCC 2220
Db 2161 AGCTCTGCCCTCCCGGGTTCGCACCACTTCTCTGCTCAGCCTCCCAATTTAGCTTGGCC 2220
Qy 2221 TACAGTCACTGCCACACACTGGCTTAAATTTTCTACTTTTCTAGTAGAGACAGGTTTC 2280
Db 2221 TACAGTCACTGCCACACACTGGCTTAAATTTTCTACTTTTCTAGTAGAGACAGGTTTC 2280
Qy 2281 ACCGTGTTAGCCAGATGGTCTCGATCTCTGACCTCGGTGATCGGCCACCTCGGCCCTCC 2340
Db 2281 ACCGTGTTAGCCAGATGGTCTCGATCTCTGACCTCGGTGATCGGCCACCTCGGCCCTCC 2340
Qy 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372
Db 2341 CAAAGTCTGGGATTTACAGGATGAGCCACCG 2372

REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 295:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-295

Query Match 9.5%; Score 226; DB 10; Length 1400;
Best Local Similarity 85.2%; Pred. No. 5e-41;
Matches 276; Conservative 0; Mismatches 45; Indels 3; Gaps 2;
QY 2050 TTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGT 2109
DB 380 TTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGT 439
QY 2110 CTTCGCTCTGTACCCAGCGTGGAGTGCAGTGG-GTGATCTTTGGCTCACTGCAAGCTCTGC 2168
DB 440 CTCGCTCTGTCCGCCAGCGTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCCGC 499
QY 2169 CTTCCCGGGTTCGCCAGCATTCCTGCTCAGCTCCCAATTAAGCTTGGCTTACAGTCA 2228
DB 500 C--TCCCGGGTTCAGCGCATTCCTGCTCAGCTCCCGGAGTACGCTGGAGTACAGGCG 557
QY 2229 TCTGCCACACACCTTGCTCAATTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGT 2288
DB 558 CCGCGCACACCGCGCGCTCAATTTTGTATTTTAGTAGAGAGCGGGTTTCACCGTGT 617
QY 2289 AGCAGGATGTCGTCGATCTCTGATCTGATCGGCCACCTCGGCCCTCCCAAGTGC 2348
DB 618 ACCAGGATGTCGTCGATCTCTGATCTGATCGGCCCGCGCTCGGCCCTCCCAAGTGC 677
QY 2349 TGGGATTACAGCGATGAGCCACCG 2372
DB 678 TGGGATTACAGCGATGAGCCACCG 701

RESULT 8
US-09-263-959-1
Sequence 1, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESS: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684973 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-263-959-1
Query Match 9.5%; Score 226; DB 10; Length 684973;
Best Local Similarity 85.2%; Pred. No. 5e-40;
Matches 276; Conservative 0; Mismatches 45; Indels 3; Gaps 2;
QY 2050 TTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGT 2109
DB 172880 TTTTCTTAAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGT 172939
QY 2110 CTTCGCTCTGTACCCAGCGTGGAGTGCAGTGG-GTGATCTTTGGCTCACTGCAAGCTCTGC 2168
DB 172940 CTCGCTCTGTCCGCCAGCGTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCCGC 172999
QY 2169 CTTCCCGGGTTCGCCAGCATTCCTGCTCAGCTCCCAATTAAGCTTGGCTTACAGTCA 2228
DB 173000 C--TCCCGGGTTCAGCGCATTCCTGCTCAGCTCCCGGAGTACGCTGGAGTACAGGCG 173057
QY 2229 TCTGCCACACACCTTGCTCAATTTTGTACTTTTAGTAGAGACAGGGTTTCACCGTGT 2288
DB 173058 CCGCGCACACCGCGCGCTCAATTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGT 173117
QY 2289 AGCAGGATGTCGTCGATCTCTGATCTGATCGGCCACCTCGGCCCTCCCAAGTGC 2348
DB 173118 AGCAGGATGTCGTCGATCTCTGATCTGATCGGCCCGCGCTCGGCCCTCCCAAGTGC 173177
QY 2349 TGGGATTACAGCGATGAGCCACCG 2372
DB 173178 TGGGATTACAGCGATGAGCCACCG 173201

RESULT 9
US-09-764-869-2110
Sequence 2110, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2110
LENGTH: 22008
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-869-2110
Query Match 9.4%; Score 223.2; DB 10; Length 22008;
Best Local Similarity 85.5%; Pred. No. 6.1e-40;
Matches 272; Conservative 0; Mismatches 43; Indels 3; Gaps 2;
QY 2056 TTAATATGATATGACATTTAAATGTAATTTATTTTGTGAGACCGAGTCTTGT 2115
DB 3451 TTAGGTAGATAGATGAGTGTGATAGATTTATTTTGTGAGACCGAGTCTTGT 3510
QY 2116 CTGTTACCCAGCGTGGAGTGCAGTGG-GTGATCTTTGGCTCACTGCAAGCTCTGCCCTCC 2174
DB 3511 CTGTTGCCAGCGTGGAGTGCAGTGGCGACGATCTCGGCCACTGCAAGCTCCAGCTT-C 3568
QY 2175 CGGGTTCCGACCATTCCTGCTCAGCTCCCAATTAAGCTTGGCTTACAGTCACTCTGCC 2234
DB 3569 CAGGTTACACACCATTCCTGCTCAGCTCCCGAGTAGCTGGGACACAGCGCCCTACC 3628

QY 2235 ACCACACCTGGCTAAATTTTGTACTTTAGTAGACAGAGGCTTACCGGTGTAGCCAG 2294
Db 3629 ACCACGCTGGCTAATTTTGTATTTTATAGTAGACAGAGGCTTACCGGTGTAGCCAG 3688
QY 2295 GATGGTCTCGATCTCCGACCTCGTATCGGCCACCTCGGCTCCCAAGTGTGGGAT 2354
Db 3689 GATGGTCTCGACCTCGTATCGGCCACCTCGGCTCCCAAGTGTGGGAT 3748
QY 2355 TACAGCATGAGCCACC 2372
Db 3749 TACAGCGTGGCCACC 3766

RESULT 10

US-09-764-877-3171
; Sequence 3171 Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3171
; LENGTH: 32185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3171

Query Match 9.4%; Score 223.2; DB 10; Length 32185;
Best Local Similarity 83.4%; Pred. No. 7e-40;
Matches 277; Conservative 0; Mismatches 53; Indels 2; Gaps 2;

QY 2041 TTGGTCTTTTCTTAATATCTATATGACATTTAAATGTAACCTATATTTTGTG 2100
Db 4482 TTTCATCTGTTTATATATATTTACTTTTAAAGTAGCTTTTATTTTGTG 4541
QY 2101 AGACAGGCTTGTCTCTTACCAGCTGGAGTGCAGTGG-GTATCTTGGCTACTGC 2159
Db 4542 AGACAGGCTTGTCTCTTACCAGCTGGAGTGCAGTGGAGTGCAGTGGCTACTGC 4601
QY 2160 AAGCTCTGCCCTCCCGGGTTCGACCATTTCTCTGCTCAGCCCTCCCAATAGCTTGGC 2219
Db 4602 AGGCTCCGCC-CCCGGGTTAGCCATTTCTCTGCTCAGCCCTCCCAATAGCTTGGG 4660
QY 2220 CTACAGTATCTGCCACACACCTGGCTAATTTTGTACTTTTGTAGACAGAGGTTT 2279
Db 4661 CTACAGGCGCCGACCTCCCGGCTAATTTTGTATTTTGTAGATGGGTTT 4720
QY 2280 CACCGTGTAGCAGGATGCTCGATCTCTGACCTCGTATCGGCCACCTCGGCTC 2339
Db 4721 CACCGTGTAGCAGGATGCTCGATCTCTGACCTCGTATCGGCCACCTCGGCTC 4780
QY 2340 CCAAGTGTGGGATTACAGCATGAGCCACC 2371
Db 4781 CCAAGTGTGGGATTACAGCGTGGAGCCACC 4812

RESULT 11

US-09-764-887-355/C
; Sequence 355 Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA113
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 355
; LENGTH: 4978
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-355

Query Match 9.4%; Score 223; DB 10; Length 4978;
Best Local Similarity 85.0%; Pred. No. 3.8e-40;
Matches 273; Conservative 0; Mismatches 45; Indels 3; Gaps 2;

QY 2052 TTTCTTAAATATGATATGACATTTAAATCTAATTTATTTTGTGAGACGAGTCT 2111
Db 2861 TGTACCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2802
QY 2112 TGTCTGTATACCCAGGCTGGAGTGCAGTGG-GTGATCTTGGCTACTGCAAGCTCTGCC 2170
Db 2801 CGCTCTGTATACCCAGGCTGGAGTGCAGTGGCGGATCTTGGCTACTGCAAGCTCTGCC 2744
QY 2171 TCCCGGGTTCGCACCAATTTCTCTGCTCAGCTCCCAATTAGCTTGGCTTACAGTCAATC 2230
Db 2743 CTCCCGGGTTCACGCCATTTCTCTGCTCAGCTCCCGAGTAGCTGGAGTACAGGCGCC 2684
QY 2231 TGCACACACCTGCTAAATTTTGTACTTTTGTAGACAGAGGTTTACCGTGTAG 2290
Db 2683 CGCCACACCGCCGGCTAATTTTGTATTTTGTAGACAGGAGTTTACCGTGTAG 2624
QY 2291 CCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTCGGCTTCCCAAGTCTG 2350
Db 2623 CCAGATGCTCTGATCTCTGACCTGCTGATCCGCCACCTCGGCTTCCCAAGTCTG 2564
QY 2351 GGATTACAGCATGAGCCACC 2371
Db 2563 GGATTACAGCGTGGAGCCACC 2543

RESULT 12

US-09-861-846-3
; Sequence 3 Application US/09861846
; Patent No. US20020110852A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001065
; CURRENT APPLICATION NUMBER: US/09/861,846
; PRIOR FILING DATE: 2001-05-22
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 13608
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(13608)
; OTHER INFORMATION: n = A,T,C or G
US-09-861-846-3

Query Match 9.4%; Score 222; DB 10; Length 13608;
Best Local Similarity 90.3%; Pred. No. 9.3e-40;
Matches 260; Conservative 0; Mismatches 25; Indels 3; Gaps 2;

QY 2086 TTATTTATTTTGTGAGACGAGTCTTGTCTGTATACCCAGGCTGGAGTGG-GTG 2144
Db 6767 TTTTATTTTGTGAGACGAGTCTTGTCTGTCTGCGAGGCTGGAGTGGAGTGGGCT 6826
QY 2145 ATCTTGGCTCACTGCAAGCTCTGCCCTCCCGGGTTCGACCATTTCTCTCCCTCAGCT 2204
Db 6827 ATCTTGGCTCACTGCAAGCTCTGCC--TCCAGGTTTACGCCATTTCTCTCCCTCAGCT 6884

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QY 2205 CCCAATTAGCTTGGCTCAGTCAATGCCACACACCTGGCTAAATTTTGTACTTTTA 2264
||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Db 6885 CCCAAGTAGCTAGGACTACAGGCGCTGCCACAGGCTGGCTAAATTTTGTACTTTTA 6944
||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
QY 2265 GTAGAGACAGGGTTTACCGTGTAGCCAGGATGCTCGATCTCCCTGACCTCGATGCC 2324
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6945 GTAGAGACAGGGTTTACCATGTTAGCCAGGATGCTCGATCTCCCTGACCTCGATGCC 7004
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2325 CCCACCTCGCGCTCCCAAGTCTGGGATTACAGGATGAGCCACCG 2372
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7005 GCTGCGCTCGCGCTCCCAAGTCTGGGATTACAGGATGAGCCACCG 7052
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13
US-09-816-685-3
; Sequence 3, Application US/09816685
; Patent No. US20020053091A1
; GENERAL INFORMATION:
; APPLICANT: CHANDRAMOULISWARAN, Ishwar et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: CL000856
; CURRENT APPLICATION NUMBER: US/09/816,685
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 41104
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(41104)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-685-3

Query Match 9.4%; Score 222; DB 10; Length 41104;
Best Local Similarity 83.8%; Pred. No. 1.4e-39;
Matches 275; Conservative 0; Mismatches 50; Indels 3; Gaps 2;

QY 2046 TTTTTCCTTAATATGATATGATGACATTTAAATGTAACATTAATTTTGTAGACC 2105
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12450 TTTGCGGTGAAATTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 12509
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2106 GAGTCTGCTCTGTATACCCAGGCTGAGTGCAGTGG-CTGATCTTGCTCAGTGCAGCT 2164
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12510 GAGTCTGCTCTGTGCGCCAGGCTGAGTGCAGTGGCGGATCTCGGCTCACTGCAAGCT 12569
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2165 CTGCGCTCCCGGGTTCGCCACCAATCTCTGCTCAGCTCCCAATTTAGCTGGCTACA 2224
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12570 CGGCG--TTCGGGGTTTACGCCCAATCTCTGCTCAGCTCCCAATTTAGCTGGCTACA 12627
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2225 GTATCTGCCACCACTGGCTGCTAAATTTTGTACTTTTAGTAGAGACAGGGTTTCACCG 2284
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12628 GCGCGCCGCCACTACGCCCGGCTAAATTTTGTACTTTTAGTAGAGACAGGGTTTCACCG 12687
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2285 TCTTAGCCAGGATGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 2344
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12688 TCTTAGCCAGGATGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 12747
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2345 GTGCTGGGATTACAGGATGAGCCACCG 2372
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 12748 GTGCTGGGATTACAGGATGAGCCACCG 12775
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 14
US-09-764-869-2355
; Sequence 2355, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

Query Match 9.4%; Score 221.8; DB 10; Length 32190;
Best Local Similarity 88.2%; Pred. No. 1.4e-39;
Matches 253; Conservative 0; Mismatches 32; Indels 2; Gaps 1;

QY 2086 TTAATATTTTITGAGACCGAGTCTTGCTCTGTATCCACCGGCTGGAGTGCAGTGGGTGA 2145
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2355
; LENGTH: 15714
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (6476)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (12084)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-2355

Query Match 9.4%; Score 221.8; DB 10; Length 15714;
Best Local Similarity 83.4%; Pred. No. 1.1e-39;
Matches 276; Conservative 0; Mismatches 52; Indels 3; Gaps 2;

QY 2043 GGTTCCTTTTCTTAAATATGATATGACATTTAAATGTAACATTAATTTTGTAG 2102
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2431 GGTTCCTTATTTATTTATTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 2490
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2103 ACCGAGTCTGCTCTGTATCCACAGGCTGGAGTGCAGTGG-CTGATCTTGGCTCACTGCAA 2161
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2491 ACGGAGTCTGCTCTGTGCGCCAGGCTGGAGTGCAGTGGCGGATCTCGGCTCACTGCAA 2550
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2162 GCTCTGCCCTCCCGGGTTCGCACCAATCTCTGCTCAGCTCCCAATTTAGCTTGGCT 2221
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2551 GCTC--CACCTCCCGGGTTCACGCCAATCTCTGCTCAGCTCCCAATTTAGCTTGGCT 2608
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2222 ACAGTCACTTCCACACACACTGGCTAAATTTTGTACTTTTAGTAGAGACAGGGTTTCA 2281
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2609 ACAGCGCCCGCCACTACGCCGGCTAAATTTTGTACTTTTAGTAGAGACAGGGTTTCA 2668
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2282 CCGTGTAGCAGAGTGTCTGATCTCTGACCTCGTGTATCCGCCACCTCGGGCTCC 2341
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2669 CCGTGTAGCAGAGTGTCTGATCTCTGACCTCGTGTATCCGCCACCTCGGGCTCC 2728
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2342 AAAGTGTGGGATTACAGGATGAGCCACCG 2372
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2729 AAAGTGTGGGATTACAGGATGAGCCACCG 2759
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-764-878-201
; Sequence 201, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 32190
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-201
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